

STIC-Biotech/ChemLib

118065

From: Chan, Christina
Sent: Monday, March 29, 2004 11:10 AM
To: Yaen, Christopher; STIC-Biotech/ChemLib
Subject: RE: 09883848-RUSH

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Yaen, Christopher
Sent: Monday, March 29, 2004 11:01 AM
To: Chan, Christina
Subject: 09883848-RUSH

Hi Christina,

could you please rush the following search:

sequence search on seq id 15, include sequences that are at least 60% identical

thanks

Christopher Yaen
US Patent Office
Art Unit 1642
571-272-0838
REM 3A20
REM 3C18

RECEIVED
MAR 29 2004
STIC

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 3/30
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

| | |
|--|--|
| or send an email to license@isb-sib.ch). | |
| CC | EMBL; U26349; AAA85163.1; -- |
| CC | HSSP; Q62226; 1VHH. |
| DR | MEROPS; C46.UPW; -- |
| DR | InterPro; IPR009045; Hedgehog/DD_pept. |
| DR | InterPro; IPR003587; Hedgehog_hint_N. |
| DR | InterPro; IPR003586; Hedgehog_hintC. |
| DR | InterPro; IPR000320; HH_signal. |
| DR | InterPro; IPR006141; Intein_S. |
| DR | InterPro; IPR001767; Pept_C46_hint. |
| DR | InterPro; IPR001657; Peptidase_C46. |
| DR | Pfam; PF01085; HH_signal; 1. |
| DR | Pfam; PF01079; Hint; 1. |
| DR | PRINTS; PR00632; SONICHOG. |
| DR | ProDom; PD003042; HH_signal; 1. |
| DR | SMART; SM00305; HintC; 1. |
| DR | SMART; SM00306; HintN; 1. |
| DR | PROSITE; PS50817; INTEIN_N_TER; 1. |
| KW | Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; |
| KW | Signal; Lipoprotein; Palmitate. |
| FT | SIGNAL 1 22 POTENTIAL. |
| FT | CHAIN 23 396 DESERT HEDGEHOG PROTEIN 1. |
| FT | CHAIN 23 197 DESERT HEDGEHOG PROTEIN 1 N-PRODUCT. |
| FT | CHAIN 198 396 DESERT HEDGEHOG PROTEIN 1 C-PRODUCT. |
| FT | DOMAIN 276 279 POLY-SER. |
| FT | SITE 197 198 CLEAVAGE (AUTO-) (BY SIMILARITY). |
| FT | SITE 267 267 INVOLVED IN AUTO-CLEAVAGE (BY |
| FT | ACT_SITE 270 270 ESSENTIAL FOR AUTO-CLEAVAGE (BY |
| FT | LIPID 23 23 N-palmitoyl cysteine (By similarity). |
| FT | LIPID 197 197 Cholesterol glycine ester (By |
| FT | SEQUENCE 396 AA; 44087 MW; 774A3EC2268A5EE9 CRC64; |
| Query Match 43.7%; Score 1079.5; DB 1; Length 396; | |
| Best Local Similarity 50.1%; Pred. No. 1.2e-70; | |
| Matches 222; Conservative 55; Mismatches 109; Indels 57; Gaps 6; | |
| QY | 6 RCLLLVLSLLVCSGLACGPRG-FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEG 64 |
| Db | 5 RIVILAICGGLLVPRCCGPRGPVGRVRRYMRKLVPLHYKQFVPNPVPEKTLGASGKSEG 64 |
| QY | 65 KISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQCKDKLNALAISVMNQWPGVKLRV 124 |
| Db | 65 KIHRGSERFIELVPNYPNDIIFKDEEKTGADRLMTERCKDRVNALAISVMNQWPGVKLRV 124 |
| QY | 125 TEGWDEDGHHSESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAHIHCS 184 |
| Db | 125 TEGWDEDGHHHAHDSLHYEGRALDITTSDDRNKYGMLARLAVEAGFDWVYYESKAHIHVS 184 |
| QY | 185 VKAENSVAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLDR 244 |
| Db | 185 VKADNSLGVRSGGCGPGTAMVMVMGTGERKPLSELKIGDVTYTTDETQGLITSVVLFLHR 244 |
| QY | 245 DDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRAL 304 |
| Db | 245 NPVKTATFVLIEAEGHPSKLLVTPNHLLFI-----QSSSAGFLP-----T 285 |
| QY | 305 FASVRPQQRVYVVAERDCGRLLPAAVHVSVTLSSEAGAYAPLTAQGTILINRVLASCY 364 |
| Db | 286 FAYRVIQIDLVIYV--NGTQVQSSKVRVSL-EEQTGVYAPMTEHGTLTLDVGLVTSY 341 |
| QY | 365 AVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGSDGGDRGGGGRVALTAPGAADAP 424 |
| Db | 342 ATVESHTLAHVS LAPRLRFQGIASML-----P 368 |
| QY | 425 GAGATAGIHWYSQLLYQIGTWLL 447 |
| Db | 369 DLMSDGVHWYCHILYVLAKYVL 391 |

| | |
|---|--|
| RESULT 17 | |
| DHH2_XENLA | STANDARD; PRT; 398 AA. |
| AC | Q91611; |
| DT | 15-JUL-1999 (Rel. 38, Created) |
| DT | 15-JUL-1999 (Rel. 38, Last sequence update) |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) |
| DE | Desert hedgehog protein precursor 2 (DHH-2) (Hedgehog protein 4) (X-HH4). |
| DE | HH4. |
| GN | Xenopus laevis (African clawed frog). |
| OS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; |
| OC | Xenopodinae; Xenopus. |
| OX | NCBI_TaxID=8355; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=Embryo; |
| RX | MEDLINE=95401852; PubMed=7671800; |
| RA | EKKER S.C., McGREW L.L., LAI C.-J., LEE J.J., von KESSLER D.P., |
| RA | MOON R.T., BEACHY P.A.; |
| RT | "Distinct expression and shared activities of members of the hedgehog |
| RT | gene family of Xenopus laevis."; |
| RL | Development 121:2337-2347(1995). |
| CC | -!- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF |
| CC | ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC |
| CC | CEMENT GLAND FORMATION IN EMBRYOS. |
| CC | -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE |
| CC | CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE |
| CC | CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED |
| CC | OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY |
| CC | SIMILARITY). |
| CC | -!- PTM: The C-terminal domain displays an autoproteolysis activity |
| CC | and a cholesterol transferase activity. Both activities result in |
| CC | the cleavage of the full-length protein and covalent attachment of |
| CC | a cholesterol moiety to the C-terminal of the newly generated N- |
| CC | terminal fragment (N-product). This covalent modification appears |
| CC | to play an essential role in restricting the spatial distribution |
| CC | of the protein activity to the cell surface. The N-product is the |
| CC | active species in both local and long-range signaling, whereas the |
| CC | C-product has no signaling activity (By similarity). |
| CC | -!- SIMILARITY: Belongs to the hedgehog family. |
| CC | ----- |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration |
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| CC | the European Bioinformatics Institute. There are no restrictions on its |
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| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ |
| CC | or send an email to license@isb-sib.ch). |
| CC | ----- |
| EMBL; U26350; AAA85164.1; -- | |
| HSSP; Q62226; 1VHH. | |
| MEROPS; C46.UPW; -- | |
| InterPro; IPR009045; Hedgehog/DD_pept. | |
| InterPro; IPR003587; Hedgehog_hint_N. | |
| InterPro; IPR003586; Hedgehog_hintC. | |
| InterPro; IPR000320; HH_signal. | |
| InterPro; IPR001767; Pept_C46_hint. | |
| InterPro; IPR001657; Peptidase_C46. | |
| Pfam; PF01085; HH_signal; 1. | |
| Pfam; PF01079; Hint; 1. | |
| PRINTS; PR00632; SONICHOG. | |
| ProDom; PD003042; HH_signal; 1. | |
| SMART; SM00305; HintC; 1. | |
| SMART; SM00306; HintN; 1. | |
| Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; | |
| Signal; Lipoprotein; Palmitate. | |
| SIGNAL 1 23 POTENTIAL. | |
| CHAIN 24 398 DESERT HEDGEHOG PROTEIN 2. | |
| CHAIN 24 199 DESERT HEDGEHOG PROTEIN 2 N-PRODUCT. | |
| CHAIN 200 398 DESERT HEDGEHOG PROTEIN 2 C-PRODUCT. | |
| DOMAIN 278 281 POLY-SER. | |

| | | | | |
|--|---|---|-------------------------------------|--|
| FT | SITE | 199 | 200 | CLEAVAGE (AUTO-) (BY SIMILARITY). |
| FT | SITE | 269 | 269 | INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | ACT_SITE | 272 | 272 | ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | LIPID | 24 | 24 | N-palmitoyl cysteine (By similarity). |
| FT | LIPID | 199 | 199 | Cholesterol glycine ester (By similarity). |
| SQ | SEQUENCE | 398 AA; 44458 MW; DBC23AF85F69DD08 CRC64; | | |
| Query Match | | | | |
| Best Local Similarity 43.6%; Score 1077.5; DB 1; Length 398; | | | | |
| Matches 221; Conservative 58; Mismatches 102; Indels 73; Gaps 7; | | | | |
| QY | 1 | MLLLARC--- | LLLVSSLLVCSGLACGPRG-- | FGKRRHPKKLTPLAYKQFIPNVAEKT 55 |
| DB | 6 | ILILAACCCWLLLLPVR----- | CCGPRGPVGRRRMRRLVPLLYKQFVNPVPEKT 57 | |
| QY | 56 | LGASGRYEGKISRNSRPFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI | SVMN 115 | |
| DB | 58 | LGASGKSEGIKRRGSERFIKLPVNPYPNDIIFKDEENTGADRLMTQRCCKDRVNALAI | SVMN 117 | |
| QY | 116 | QWPGVKLRVTEGDEDEHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVY | 175 | |
| DB | 118 | MWPGKLRVTEGDEDEGHAHDSLHYEGRALDITTSDDRNKYGMLARLAVEAGFDWVY | 177 | |
| QY | 176 | ESKAHHCVSVAENSVAAKSGCGFCPSATVHLEGGTKLVKDLSPGDRVLAADDQGRLLY | 235 | |
| DB | 178 | ESKAHHSVNTDNSLVSRCGFCPGTAMVMETGKKPLSELKLGDTVFTTDETGLLIH | 237 | |
| QY | 236 | SDFLTFLDRDDGAKKVFVVIETREPRERLLLTAAHLFVAPHNDSATGEPEASSGSGPPS | 295 | |
| DB | 238 | SVLLFLHRDPYKATATFVLEAEGHPTKLLVTPNHLFI----- | KS 278 | |
| QY | 296 | GGALCPRALFASRVPRGQ--RVYVVAERDGRRLPAAVHSVLTSEEAAGAYAPLTAQGT | 353 | |
| DB | 279 | SSSTGFQPTFAIRVQIGDLIQIYVNGTQVSSKVRVSV----- | DEQTGYAPMTEHGT 332 | |
| QY | 354 | ILINRVLASCYAVIEEHSWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGGRV | 413 | |
| DB | 333 | LLVDGVLTSYATVESHITLHASLAPRLRFGIASML----- | 369 | |
| QY | 414 | ALTAPGAADAPGAGATAGIHWISQLLYQIGTWLL | 447 | |
| DB | 370 | ----- | PDLHTSDGVHWHYCHILYVLAKYVL 393 | |
| RESULT 18 | | | | |
| HH | HH | DROME | STANDARD; | PRT; 421 AA. |
| AC | Q02936; | Q9VCQ4; | | |
| DT | 01-FEB-1994 | (Rel. 28, Created) | | |
| DT | 15-MAR-2004 | (Rel. 43, Last sequence update) | | |
| DT | 15-MAR-2004 | (Rel. 43, Last annotation update) | | |
| DE | Hedgehog protein precursor. | | | |
| CN | HH | OR | CG4637. | |
| OS | Drosophila melanogaster (Fruit fly). | | | |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; | | | |
| OC | Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; | | | |
| OC | Ephydroidea; Drosophilidae; Drosophila. | | | |
| OX | NCBI_TaxID=7227; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM LONG), FUNCTION, DEVELOPMENTAL STAGE, AND | | | |
| RP | TISSUE SPECIFICITY. | | | |
| RC | STRAIN=Canton-S; TISSUE=Embryo; | | | |
| RX | MEDLINE=93185922; PubMed=8166882; | | | |
| RA | Takahashi S., Michiue T., Higashijima S.-I., Zenno S., Ishimaru S., | | | |
| RA | Takahashi F., Orihara M., Kojima T., Saigo K.; | | | |
| RT | "Structure and expression of hedgehog, a Drosophila segment-polarity | | | |
| RT | gene required for cell-cell communication."; | | | |
| RL | Gene 124:183-189(1993). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM LONG), FUNCTION, DEVELOPMENTAL STAGE, AND | | | |

| | | | | |
|----|--|--|--|--|
| RP | TISSUE SPECIFICITY. | | | |
| RX | MEDLINE=93008241; PubMed=1394430; | | | |
| RA | Lee J.J., von Kessler D.P., Parks S., Beachy P.A.; | | | |
| RT | "Secretion and localized transcription suggest a role in positional | | | |
| RT | signaling for products of the segmentation gene hedgehog."; | | | |
| RL | Cell 71:33-50(1992). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A., ALTERNATIVE SPLICING, SUBCELLULAR LOCATION, | | | |
| RP | DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY. | | | |
| RC | TISSUE=Embryo; | | | |
| RX | MEDLINE=93083438; PubMed=1280560; | | | |
| RA | Mohler J., Vani K.; | | | |
| RT | "Molecular organization and embryonic expression of the hedgehog gene | | | |
| RT | involved in cell-cell communication in segmental patterning of | | | |
| RT | Drosophila."; | | | |
| RL | Development 115:957-971(1992). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM LONG), FUNCTION, DEVELOPMENTAL STAGE, AND | | | |
| RP | TISSUE SPECIFICITY. | | | |
| RC | STRAIN=Oregon-R; TISSUE=Embryo; | | | |
| RX | MEDLINE=94040725; PubMed=1340474; | | | |
| RA | Tabata T., Eaton S., Kornberg T.B.; | | | |
| RT | "The Drosophila hedgehog gene is expressed specifically in posterior | | | |
| RT | compartment cells and is a target of engrailed regulation."; | | | |
| RL | Genes Dev. 6:2635-2645(1992). | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | STRAIN=Berkeley; | | | |
| RX | MEDLINE=20196006; PubMed=10731132; | | | |
| RA | Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., | | | |
| RA | Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., | | | |
| RA | George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., | | | |
| RA | Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., | | | |
| RA | Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., | | | |
| RA | Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., | | | |
| RA | Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., | | | |
| RA | Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., | | | |
| RA | Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., | | | |
| RA | Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., | | | |
| RA | Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., | | | |
| RA | Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., | | | |
| RA | de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., | | | |
| RA | Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., | | | |
| RA | Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., | | | |
| RA | Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., | | | |
| RA | Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., | | | |
| RA | Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Hough J., | | | |
| RA | Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A., | | | |
| RA | Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z., | | | |
| RA | Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Liang Y., Lin X., | | | |
| RA | Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., McPherson D., | | | |
| RA | Liu X., Mattel B., McIntosh T.C., McLeod M.P., Moshrefi A., | | | |
| RA | Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., | | | |
| RA | Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., | | | |
| RA | Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., | | | |
| RA | Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., | | | |
| RA | Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., | | | |
| RA | Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., | | | |
| RA | Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., | | | |
| RA | Swirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X., | | | |
| RA | Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., | | | |
| RA | Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., | | | |
| RA | Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., | | | |
| RA | Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., | | | |
| RT | Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; | | | |
| RT | "The genome sequence of Drosophila melanogaster."; | | | |
| RL | Science 287:2185-2195(2000). | | | |
| RN | [6] | | | |
| RP | AUTOPROTEOLYTIC CLEAVAGE. | | | |
| RX | MEDLINE=95191685; PubMed=7885476; | | | |
| RA | Porter J.A., von Kessler D.P., Ekker S.C., Young K.E., Lee J.J., | | | |
| RA | Moses K., Beachy P.A.; | | | |
| RT | "The product of hedgehog autoproteolytic cleavage active in local and | | | |

DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hedgehog protein precursor.
GN HH.
OS Drosophila hydei (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, genetic linkage and limb patterning activity of a murine
RT hedgehog gene."
RL Development 120:3339-3353(1994).
CC -!- FUNCTION: Intercellular signal essential for a variety of
CC patterning events during development. Establishes the anterior-
CC posterior axis of the embryonic segments and patterns the larval
CC imaginal disks. Binds to the patched (ptc) receptor, which
CC functions in association with smoothened (smo), to activate the
CC transcription of target genes wingless (wg), decapentaplegic (dpp)
CC and ptc. In the absence of hh, ptc represses the constitutive
CC signaling activity of smo through fused (fu).
CC -!- SUBCELLULAR LOCATION: C-terminal peptide diffuses from the cell,
CC the N-terminal peptide remains associated with the cell surface.
CC Also secreted in either cleaved or uncleaved form to mediate
CC signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length hedgehog protein and covalent
CC attachment of a cholesterol moiety to the C-terminal of the newly
CC generated amino-terminal fragment (N-product). This covalent
CC modification appears to play an essential role in restricting the
CC spatial distribution of the hedgehog activity to the cell surface.
CC Amino-terminal palmitoylation of hedgehog N-product is required
CC for the embryonic and larval patterning activities of the hedgehog
CC signal. The N-product is the active species in both local and
CC long-range signaling, whereas the C-terminal product has no
CC signaling activity (By similarity).
CC -!- PTM: Ras acts within the secretory pathway to catalyze the N-
CC terminal palmitoylation of Hh (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
DR HSP; Q02936; 1A70.
DR MEROPS; C46.001; -.
DR FlyBase; FBgn0015646; Dhyd\hh.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR003586; Hedgehog_hint_C.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
KW Hydrolase; Protease; Developmental protein;
KW Segmentation polarity protein; Signal; Autocatalytic cleavage;
KW Lipoprotein; Palmitate.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 422 HEDGEHOG PROTEIN.
FT CHAIN 32 205 HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 206 422 HEDGEHOG PROTEIN C-PRODUCT.
FT SITE 205 206 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT SITE 251 251 INVOLVED IN CHOLESTEROL TRANSFER (BY
FT SIMILARITY).
FT SITE 274 274 INVOLVED IN AUTO-CLEAVAGE (BY
FT SIMILARITY).

FT ACT_SITE 277 277 ESSENTIAL FOR AUTO-CLEAVAGE (BY
FT SIMILARITY).
FT LIPID 32 32 N-palmitoyl cysteine (By similarity).
FT LIPID 205 205 Cholesterol glycine ester (By
FT similarity).
SQ SEQUENCE 422 AA; 47407 MW; BEB63B1BE4729DB5 CRC64;
Query Match 34.6%; Score 854; DB 1; Length 422;
Best Local Similarity 44.3%; Pred. No. 2.4e-54;
Matches 198; Conservative 65; Mismatches 142; Indels 42; Gaps 10;
QY 8 LLLVLVSSLLVCSGLACGPGRGFGKRRHPKKTLPAYKQFIPNVAEKTGLGASGRYEGKIS 67
DB 16 LLLLLLLALNFRHAHSCGPGRLGRRRE-RNLFPLVLKQTVPNLSEVHNSASGPLEGAIQ 74
QY 68 RNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAISVMNQMPGVKLRVTEG 127
DB 75 RDSPKFKNLVLNPNRDIEFRDEEGTGADRVMSKRCREKLNMLAYSVMNEWPGVRLRVTES 134
QY 128 WDEGDHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHIHCSVKA 187
DB 135 WDEDRHQGESLHYEGRAVTIATSDHDQSKYGMARLAVEAGFDWVSVRRHIYCSVKS 194
QY 188 ENSVA-AKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRDD 246
DB 195 DSSPSISHMHGCFPESTALLESAGAEKALGELAGDRVLSMDVKGQPVYSEVILFMDRNL 254
QY 247 GAKKVYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPFGGALGPRALFA 306
DB 255 EQVENFVLHT-DGGAVLTVPALHLSV-----WQPERQT-----LNFIFA 294
QY 307 SRVRPGQRYVVAERDGDRLLPAAVHVSVTLSHEAAGAYAPLTAQCTILINRVLASCYAV 366
DB 295 DRV---EELDYVLVRDATGELQPVRLRG-SVQSRGVVAPLTREGTIVNSVAASCYAV 350
QY 367 IEHSHWAHRAFPRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGAADAPGA 426
DB 351 ISSQSLAHWGLAPMRL--STLQSWMPAK-----GQLRTAQDKSTPKDAT-A 394
QY 427 GATAGIHWYSQLLYQIGTWLLDSEALH 453
DB 395 QQQNGLHWYANALYKVDYVLPKSWRH 421

RESULT 20

SHH_RASEL STANDARD; PRT; 121 AA.
AC P79858; P79859;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Rasbora elegans (Elegant rasbora).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Rasbora.
OX NCBI_TaxID=27712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,

```
CC PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U51355; AAB38578.1; -.
CC EMBL; U51374; AAB38597.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH signal.
CC InterPro; IPR001657; Peptidase_C46.
CC PRINTS; PR00632; SONICHHOG.
CC ProDom; PD003042; HH_signal; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
CC NON_TER 1
CC NON_CONS 63 64
CC NON_TER 121 121
CC SEQUENCE 121 AA; 13975 MW; 6C9334E41C739B4F CRC64;
CC
CC Query Match 24.4%; Score 602; DB 1; Length 121;
CC Best Local Similarity 81.6%; Pred. No. 7.4e-37;
CC Matches 115; Conservative 4; Mismatches 2; Indels 20; Gaps 1;
CC
CC QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPDIIFKDE 89
CC :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC Db 1 YGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPDIIFKDE 60
CC
CC QY 90 ENTGADRLMTQRCCKDKLNALAI SVMNQWPGVKLVTEGWDGHHSEESLHYEGRAVDIT 149
CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC Db 61 ENT-----VMNQWPGVKLVTEGWDGHHFEESLHYEGRAVDIT 100
CC
CC QY 150 TSDRDRSKYGMRLARLAVEAGF 170
CC :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC Db 101 TSDRDKSKYGTLSRLAVEAGF 121
CC
CC RESULT 21
CC SHH_CARAU STANDARD; PRT; 121 AA.
CC AC P79691; P79692;
CC DT 15-JUL-1999 (Rel. 38, Created)
CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE Sonic hedgehog protein (SHH) (Fragments).
CC GN SHH.
CC OS Carassius auratus (Goldfish).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
CC OC Cyprinidae; Carassius.
CC OX NCBI_TaxID=7957;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Muscle;
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RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
CC PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U51356; AAB38565.1; -.
CC EMBL; U51375; AAB38583.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH signal.
CC InterPro; IPR001657; Peptidase_C46.
CC PRINTS; PR00632; SONICHHOG.
CC ProDom; PD003042; HH_signal; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
CC NON_TER 1
CC NON_CONS 63 64
CC NON_TER 121 121
CC SEQUENCE 121 AA; 14003 MW; 559334E4057391C1 CRC64;
CC
CC Query Match 24.3%; Score 599; DB 1; Length 121;
CC Best Local Similarity 80.9%; Pred. No. 1.2e-36;
CC Matches 114; Conservative 5; Mismatches 2; Indels 20; Gaps 1;
CC
CC QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPDIIFKDE 89
CC :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC Db 1 YGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPDIIFKDE 60
CC
CC QY 90 ENTGADRLMTQRCCKDKLNALAI SVMNQWPGVKLVTEGWDGHHSEESLHYEGRAVDIT 149
CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC Db 61 ENT-----VMNQWPGVKLVTEGWDGHHFEESLHYEGRAVDIT 100
CC
CC QY 150 TSDRDRSKYGMRLARLAVEAGF 170
CC :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
CC Db 101 TSDRDKSKYGTLSRLAVEAGF 121
CC
CC RESULT 22
CC SHH_PUNTE STANDARD; PRT; 121 AA.
CC ID SHH_PUNTE
CC AC P79850; P79851;
CC DT 15-JUL-1999 (Rel. 38, Created)
```

DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Puntius tetrazona (Tiger barb).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Puntius.
OX NCBI_TaxID=27709;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
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CC -----
DR EMBL; U51352; AAB38577.1; -.
DR EMBL; U51371; AAB38596.1; -.
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR00320; HH_signal.
DR InterPro; IPR01657; Peptidase_C46.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 64
FT NON_CONS 63 64
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 14003 MW; 559334E4057391C1 CRC64;

Query Match 24.3%; Score 599; DB 1; Length 121;
Best Local Similarity 80.9%; Pred. No. 1.2e-36;
Matches 114; Conservative 5; Mismatches 2; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQIPNVAEKTGLGASGRYEGKISNSERFKELTPNYPNPIIFKDE 89
:|:|||||
DB 1 YGRRRHPKLTPLAYKQIPNVAEKTGLGASGRYEGKITNSERFKELTPNYPNPIIFKDE 60
:|:|||||
QY 90 ENTGADRLMTQRCKDKLNALISVMNQWPGVKLRVTEGDEGHHSEESLHYEGRAVDIT 149
:|:|||||

Db 61 ENT-----VMNQWPGVKLRVTEGDEGHHSEESLHYEGRAVDIT 100
QY 150 TSDRDRSKYGMRLARLAVEAGF 170
:|:|||||:|:|||||
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 23
SHH_RASHE
ID SHH_RASHE STANDARD; PRT; 121 AA.
AC P79864; P79865;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Rasbora heteromorpha (Rasbora).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Rasbora.
OX NCBI_TaxID=30731;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
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CC -----
DR EMBL; U51354; AAB38579.1; -.
DR EMBL; U51372; AAB38598.1; -.
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR00320; HH_signal.
DR InterPro; IPR01657; Peptidase_C46.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 64
FT NON_CONS 63 64
FT NON_TER 121 121


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SQ SEQUENCE 121 AA; 13940 MW; 6C9334EA1C73954F CRC64;
Query Match 24.2%; Score 598; DB 1; Length 121;
Best Local Similarity 80.9%; Pred. No. 1.4e-36;
Matches 114; Conservative 5; Mismatches 2; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPNDIIFKDE 89
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 YGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPNDIIFKDE 60

QY 90 ENTGADRLMTQRCCKLNALAISVMNQWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDIT 149
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ENT-----VNMQWPGVKLRVTEGWDEDDGHLEESLHYKGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 24
SHH_RASPA
ID SHH_RASPA STANDARD; PRT; 121 AA.
AC P79869; P79870;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Rasbora paviei (Sidel stripe rasbora).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Rasbora.
OX NCBI_TaxID=38659;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
CC PTC REPRESSSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoprotoeolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
-----
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or send an email to license@isb-sib.ch).
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DR EMBL; U51343; AAB38580.1; -.
DR EMBL; U51362; AAB38599.1; -.
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_CONS 63 64
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13974 MW; 669334E406739088 CRC64;

Query Match 24.2%; Score 598; DB 1; Length 121;
Best Local Similarity 80.9%; Pred. No. 1.4e-36;
Matches 114; Conservative 5; Mismatches 2; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPNDIIFKDE 89
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 YGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPNDIIFKDE 60

QY 90 ENTGADRLMTQRCCKLNALAISVMNQWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDIT 149
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ENT-----VNMQWPGVKLRVTEGWDEDDGHFEESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 25
SHH_TANAL
ID SHH_TANAL STANDARD; PRT; 121 AA.
AC P79915; P79916;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Tanichthys albonubes (White cloud mountain minnow).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Tanichthys.
OX NCBI_TaxID=38762;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
CC PTC REPRESSSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoprotoeolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
-----
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or send an email to license@isb-sib.ch).
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Zardoya R., Abouheif E., Meyer A.;
"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish.";
Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
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RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
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SIMILARITY).
-!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
-!- PTM: The C-terminal domain displays an autotransferase activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
-!- SIMILARITY: Belongs to the hedgehog family.
-----
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-----
EMBL; U51347; AAB38567.1; -.
DR EMBL; U51366; AAB38584.1; -.
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 64
FT NON_CONS 63 64
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;

Query Match 24.1%; Score 594; DB 1; Length 121;
Best Local Similarity 80.1%; Pred. No. 2.8e-36;
Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGRRHPKLLTPLAYKQFIPNVAEKTILGASGRYEGKISRNSERFKELTPNYPDIIFKDE 89
Db 1 YGRRHPKLLTPLAYKQFIPNVAEKTILGASGRYEGKITRNSERFKELTPNYPDIIFKDE 60
QY 90 ENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGWEDDGHHSSESLHYEGRAVDIT 149
Db 61 ENT-----VMNHWPVKLRVTEGWEDDGHHSSESLHYEGRAVDIT 100
QY 150 TSDRDRSKYGMRLARLAVEAGF 170
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 28
SHH_DANAE
ID SHH_DANAE STANDARD; PRT; 121 AA.
AC O13234; O13190; O13199; O13239;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)

```

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QY 150 TSDRDRSKYGMRLARLAVEAGF 170
      |||||:|||||:|||||:|||||
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 29
SHH_DANAT STANDARD; PRT; 121 AA.
AC 013238; 013193; 013198; 013237;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Danio aff. tweediei.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=46785;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
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RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
PTC REPRESSED THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----
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CC -----
DR EMBL; U51348; AAB38568.1; -
DR EMBL; U51367; AAB38585.1; -
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_TER 63
FT NON_TER 121
FT NON_TER 121
SQ SEQUENCE 121 AA; 14012 MW; A59A2DE40573825C CRC64;
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Query Match 24.1%; Score 594; DB 1; Length 121;
Best Local Similarity 80.1%; Pred. No. 2.8e-36;
Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNPNPDIIIFKDE 89
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 YGRRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNPNPDIIIFKDE 60

QY 90 ENTGADRLMTQRCCKDKLNALAI SVMNQWPGVKLRVTEGWDGHHSESLHYEGRAVDIT 149
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ENT-----VMNHWPVGKLRVTEGWDGHHSESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
      |||||:|||||:|||||:|||||
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 30
SHH_DANFR STANDARD; PRT; 121 AA.
AC 013245; 013208; 013209; 013246;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Danio frankei (Leopard danio) (Brachydanio rerio frankei).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=27702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
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NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
PTC REPRESSED THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----
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CC -----
DR EMBL; U51339; AAB38570.1; -
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DR EMBL; U51357; AAB38588.1; -.
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_CONS 63 64
FT NON_TER 121
SQ SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;

Query Match      24.1%; Score 594; DB 1; Length 121;
Best Local Similarity 80.1%; Pred. No. 2.8e-36;
Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPDIIFKDE 89
   :|:|||||
Db 1 YGRRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPDIIFKDE 60

QY 90 ENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGWDGHHSEESLHYEGRAVDIT 149
   |||
Db 61 ENT-----VMNHMPGVKLRVTEGWDGHHFEESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
   |||||:|||||
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 31
SHH_DANKE
ID SHH_DANKE STANDARD; PRT; 121 AA.
AC P79709; P79710;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Danio kerri (Kerr's danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=38750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
   closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
CC PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
```

```
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; U51340; AAB38571.1; -.
CC EMBL; U51359; AAB38589.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001657; Peptidase_C46.
CC PRINTS; PR00632; SONICHOG.
CC ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_CONS 63 64
FT NON_TER 121
SQ SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;

Query Match      24.1%; Score 594; DB 1; Length 121;
Best Local Similarity 80.1%; Pred. No. 2.8e-36;
Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPDIIFKDE 89
   :|:|||||
Db 1 YGRRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPDIIFKDE 60

QY 90 ENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGWDGHHSEESLHYEGRAVDIT 149
   |||
Db 61 ENT-----VMNHMPGVKLRVTEGWDGHHFEESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
   |||||:|||||
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 32
SHH_DANPU
ID SHH_DANPU STANDARD; PRT; 121 AA.
AC P79717; P79718;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Danio pulcher.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=38751;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
   closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
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CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
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CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
CC PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
CC SIMILARITY).
```


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CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----
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CC -----

DR EMBL; U51342; AAB38573.1; -.
DR EMBL; U51361; AAB38591.1; -.
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 64
FT NON_CONS 63 64
FT NON_TER 121 121
FT SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;

Query Match 24.1%; Score 594; DB 1; Length 121;
Best Local Similarity 80.1%; Pred. No. 2.8e-36;
Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPDIIIFKDE 89
Db 1 YGRRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPDIIIFKDE 60

QY 90 ENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGWDEDEGHHSSESLHYEGRAVDIT 149
Db 61 ENT-----VMNHWPGVKLRVTEGWDEDEGHHSSESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
Db 101 TSDRDRSKYGTLSRLAVEAGF 121

RESULT 33
SHH_DEVMA STANDARD; PRT; 121 AA.
ID SHH_DEVMA STANDARD; PRT; 121 AA.
AC O13241; O13203; O13204; O13242;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Devario devario (Danio devario).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=46781;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;

RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
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CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
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CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
CC and a cholesterol transferase activity. Both activities result in
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CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----

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CC -----

DR EMBL; U51350; AAB38569.1; -.
DR EMBL; U51369; AAB38587.1; -.
DR HSSP; Q62226; 1VHH.

DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PR00632; SONICHHOG.

DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.

FT NON_TER 1 64
FT NON_CONS 63 64
FT NON_TER 121 121
FT SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;

Query Match 24.1%; Score 594; DB 1; Length 121;
Best Local Similarity 80.1%; Pred. No. 2.8e-36;
Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPDIIIFKDE 89
Db 1 YGRRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPDIIIFKDE 60

QY 90 ENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGWDEDEGHHSSESLHYEGRAVDIT 149
Db 61 ENT-----VMNHWPGVKLRVTEGWDEDEGHHSSESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
Db 101 TSDRDRSKYGTLSRLAVEAGF 121

RESULT 34
SHH_DEVMA STANDARD; PRT; 121 AA.
ID SHH_DEVMA STANDARD; PRT; 121 AA.
AC O13247; O13213; O13214; O13248;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Sonic hedgehog protein (SHH) (Fragments).

GN SHH.

OS Devario malabaricus (Danio malabaricus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=46780;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RX MEDLINE=97075114; PubMed=8917540;

RA Zardoya R., Abouheif E., Meyer A.;

RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."

RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).

CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).

CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).

CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC EMBL; U51346; AAB38572.1; -

CC EMBL; U51365; AAB38590.1; -

CC HSSP; Q62226; 1VHH.

CC InterPro; IPR009045; Hedgehog/DD_pept.

CC InterPro; IPR00320; HH signal.

CC InterPro; IPR001657; Peptidase_C46.

CC PRINTS; PR00632; SONICHOG.

CC ProDom; PD003042; HH_signal; 1.

KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.

FT NON_TER 1

FT NON_CONS 63 64

FT NON_TER 121 121

SQ SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;

Query Match 24.1%; Score 594; DB 1; Length 121;

Best Local Similarity 80.1%; Pred. No. 2.8e-36;

Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQIPNVAEKTIGASGRYEGKISRNSERFKELTPNYPDIIFKDE 89

Db :|||||

QY 90 ENTGADRLMTQRCCKDKLNALAI SVMNQWPGVKLRVTEGWDGDGHHSERSLHYEGRAVDIT 149

Db |||

QY 61 ENT-----VMNHWPVKLRVTEGWDGDGHHPESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170

Db |||||:|||||:|||||

101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 35

SHH_DEVPA STANDARD; PRT; 121 AA.

AC O13250; O13218; O13219; O13251;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Sonic hedgehog protein (SHH) (Fragments).

GN SHH.

OS Devario pathirana (Barred danio) (Danio pathirana).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=46779;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RX MEDLINE=97075114; PubMed=8917540;

RA Zardoya R., Abouheif E., Meyer A.;

RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."

RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).

CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).

CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).

CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC EMBL; U51345; AAB38574.1; -

CC EMBL; U51364; AAB38592.1; -

CC HSSP; Q62226; 1VHH.

CC InterPro; IPR009045; Hedgehog/DD_pept.

CC InterPro; IPR00320; HH signal.

CC InterPro; IPR001657; Peptidase_C46.

CC PRINTS; PR00632; SONICHOG.

CC ProDom; PD003042; HH_signal; 1.

KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.

FT NON_TER 1

FT NON_CONS 63 64

FT NON_TER 121 121

SQ SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;

```
Query Match      24.1%; Score 594; DB 1; Length 121;
Best Local Similarity 80.1%; Pred. No. 2.8e-36;
Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPNDIIFKDE 89
Db 1 YGRRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPNDIIFKDE 60

QY 90 ENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGDEGHHSEESLHYEGRAVDIT 149
Db 61 ENT-----VMNHWPVGKLRVTEGDEGHHFEESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 36
SHH_PUNCO
ID SHH_PUNCO STANDARD; PRT; 121 AA.
AC P79838; P79840;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Puntius conchoniuss (Rosy barb).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Puntius.
OX NCBI_TaxID=27708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
PTC REPRESENTS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
-----
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or send an email to license@isb-sib.ch).
-----
CC EMBL; U51353; AAB38576.1; --
CC EMBL; U51373; AAB38595.1; --
DR
```

```
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_CONS 63
FT NON_TER 121
SQ SEQUENCE 121 AA; 14078 MW; A5832D7405738DAC CRC64;

Query Match      23.9%; Score 590; DB 1; Length 121;
Best Local Similarity 79.4%; Pred. No. 5.4e-36;
Matches 112; Conservative 6; Mismatches 3; Indels 20; Gaps 1;

QY 30 FGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISRNSERFKELTPNYPNDIIFKDE 89
Db 1 YGRRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKITRNSERFKELTPNYPNDIIFKDE 60

QY 90 ENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGDEGHHSEESLHYEGRAVDIT 149
Db 61 ENT-----VMNQWPGVKLRVTEGDEGHHFEESLHYEGRAVDIT 100

QY 150 TSDRDRSKYGMRLARLAVEAGF 170
Db 101 TSDRDKSKYGTLSRLAVEAGF 121

RESULT 37
DHH_BRARE
ID DHH_BRARE STANDARD; PRT; 88 AA.
AC P79729; Q9YGU3;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Desert hedgehog protein (DHH) (Fragment).
GN DHH.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A. PubMed=9831563;
RX MEDLINE=99051425; PubMed=8917540;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
RA Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
RA Postlethwait J.;
RA "Zebrafish hox clusters and vertebrate genome evolution."
RL Science 282:1711-1714(1998).
RN [2]
RP SEQUENCE OF 14-71 FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Intercellular signal essential for a variety of
patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide remains associated with the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
active species in both local and long-range signaling, whereas the
```



```
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF071236; AAD15931.1; -.
CC EMBL; U51388; AAB38613.1; -.
CC HSSP; Q62226; 1VHH.
CC ZFIN; ZDB-GENE-990714-5; dhh.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC PRINTS; PR00632; SONICHOG.
CC ProDom; PD003042; HH_signal; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
KW NON_TER 1
FT CONFLICT 17 17 Q -> M (IN REF. 2).
FT CONFLICT 22 22 R -> K (IN REF. 2).
FT CONFLICT 28 28 A -> G (IN REF. 2).
FT CONFLICT 34 38 HPPG -> NHLE (IN REF. 2).
FT CONFLICT 56 57 TK -> RN (IN REF. 2).
FT CONFLICT 61 61 L -> M (IN REF. 2).
FT CONFLICT 64 64 Q -> R (IN REF. 2).
FT NON_TER 88
SQ SEQUENCE 88 AA; 10069 MW; E3D34A0C36677FA6 CRC64;
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Query Match 16.0%; Score 396; DB 1; Length 88;
Best Local Similarity 81.8%; Pred. No. 3.6e-22;
Matches 72; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

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QY 100 QRCQKLNALATSVNQWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYG 159
DB 1 QRCQKCLYKLAIAVMNQWPGVRLRVTEAWDEDDGHPPGSLHYEGRAVDITTSDDRTKYG 60
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QY 160 MLARLAVEAGDWMVYVESKAHHCVSKA 187
DB 61 LLAQLAVEAGDWMVYVESKYHVHCVSKA 88
```

```
RESULT 38
ID IHH_CARAU STANDARD; PRT; 58 AA.
AC P79593;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Inter cellular signal essential for a variety of
CC patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
```

```
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U51386; AAB38601.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC PRINTS; PR00632; SONICHOG.
CC ProDom; PD003042; HH_signal; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
KW NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04D809 CRC64;
```

Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity 93.1%; Pred. No. 5.8e-15;
Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
QY 113 VMNQWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMARLAVEAGF 170
DB 1 VMNLWPGVRLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRNKYAMARLAVEAGF 58
```

```
RESULT 39
ID IHH_DANAT STANDARD; PRT; 58 AA.
AC O13240; O13200;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Danio aff. tweediei.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=46785;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Inter cellular signal essential for a variety of
CC patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
```


CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U51381; AAB38602.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC PRINTS; PR00632; SONICHHOG.
CC ProDom; PD003042; HH_signal; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
KW NON_TER 1 58
FT NON_TER 58
FT SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04D809 CRC64;
SQ

Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity 93.1%; Pred. No. 5.8e-15;
Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 113 VNMWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGF 170
DB 1 VNMWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGF 58

RESULT 40
IHH_DANKE
ID IHH_DANKE STANDARD; PRT; 58 AA.
AC P79711;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Danio kerri (Kerr's danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=38750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Inter cellular signal essential for a variety of
CC patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoprotoeolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the

CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U51376; AAB38604.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC PRINTS; PR00632; SONICHHOG.
CC ProDom; PD003042; HH_signal; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
KW NON_TER 1 58
FT NON_TER 58
FT SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04D809 CRC64;
SQ

Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity 93.1%; Pred. No. 5.8e-15;
Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 113 VNMWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGF 170
DB 1 VNMWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGF 58

RESULT 41
IHH_DANPU
ID IHH_DANPU STANDARD; PRT; 58 AA.
AC P79719;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Danio pulcher.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=38751;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
RT closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Inter cellular signal essential for a variety of
CC patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoprotoeolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; U51377; AAB38606.1; --
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04D809 CRC64;

Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity 93.1%; Pred. No. 5.8e-15;
Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 113 VMNQWPGVKLRVTEGWDGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGF 170
Db 1 VMNLWPGVRLRVTEGWDGHHSEESLHYEGRAVDITTSDDRNKYAMLARLAVEAGF 58

RESULT 42
IHH_DEVDE
ID IHH_DEVDE STANDARD; PRT; 58 AA.
AC O13243; O13205;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Devario devario (Danio devario).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=46781;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Intercellular signal essential for a variety of
patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U51382; AAB38603.1; --
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04D809 CRC64;

Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity 93.1%; Pred. No. 5.8e-15;
Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 113 VMNQWPGVKLRVTEGWDGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGF 170
Db 1 VMNLWPGVRLRVTEGWDGHHSEESLHYEGRAVDITTSDDRNKYAMLARLAVEAGF 58

RESULT 43
IHH_PUNTE
ID IHH_PUNTE STANDARD; PRT; 58 AA.
AC P79852;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Puntius tetrazona (Tiger barb).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Puntius.
OX NCBI_TaxID=27709;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Intercellular signal essential for a variety of
patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U51384; AAB38608.1; --
DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
DR Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 58
FT NON_TER 58
SQ SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04D809 CRC64;

Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity 93.1%; Pred. No. 5.8e-15;
Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 113 VMNQWPGVKLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGF 170
Db 1 VMNLWPGVRLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRNKYAMLARLAVEAGF 58

RESULT 44
IHH_RASEL STANDARD; PRT; 58 AA.
AC P79860;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Rasbora elegans (Elegant rasbora).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Rasbora.
OX NCBI_TaxID=27712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish."
Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Inter cellular signal essential for a variety of
patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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or send an email to license@isb-sib.ch).

EMBL; U51385; AAB38609.1; --
HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.

DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
DR Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 58
FT NON_TER 58
SQ SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04D809 CRC64;

Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity 93.1%; Pred. No. 5.8e-15;
Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 113 VMNQWPGVKLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGF 170
Db 1 VMNLWPGVRLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRNKYAMLARLAVEAGF 58

RESULT 45
SHH_PSEPR STANDARD; PRT; 58 AA.
AC P79839;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragment).
GN SHH.
OS Pseudorasbora parva.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Pseudorasbora.
OX NCBI_TaxID=51549;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish."
Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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EMBL; U51358; AAB38594.1; --

DR HSSP; Q62226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003020; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 58
SQ SEQUENCE 58 AA; 6608 MW; BDEAB71BD19FA6B9 CRC64;

Query Match 11.7%; Score 289; DB 1; Length 58;
Best Local Similarity 91.4%; Pred. No. 1.1e-14;
Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 113 VMNQPGVKLRVTEGWDEDEGHSESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGF 170
Db 1 VMNQPGVNLRVTEGWDEDEGHSESLHYEGRAVDITTSRDRSKYGTLSRLAVEAGF 58

RESULT 46
DHH_DANKE STANDARD; PRT; 58 AA.
AC P79712;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Desert hedgehog protein (DHH) (Fragment).
GN DHH.
OS Danio kerri (Kerr's danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=38750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Intercellular signal essential for a variety of patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoprolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC EMBL; U51387; AAB38612.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR003020; HH_signal.
CC InterPro; IPR001657; Peptidase_C46.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.

DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 58
SQ SEQUENCE 58 AA; 6657 MW; 62DBC28ABC2A5390 CRC64;

Query Match 11.7%; Score 288; DB 1; Length 58;
Best Local Similarity 91.4%; Pred. No. 1.3e-14;
Matches 53; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 113 VMNQPGVKLRVTEGWDEDEGHSESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGF 170
Db 1 VMNMWPGVKLRVTEGWDEDEGNHFEDSLHYEGRAVDITTSRDRNKYGMRLARLAVEAGF 58

RESULT 47
IHH_DEVMA STANDARD; PRT; 58 AA.
AC O13215;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Indian hedgehog protein (IHH) (Fragment).
GN IHH.
OS Devario malabaricus (Danio malabaricus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=46780;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
CC -!- FUNCTION: Intercellular signal essential for a variety of patterning events during development (By similarity).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoprolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC EMBL; U51380; AAB38605.1; -.
CC HSSP; Q62226; 1VHH.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC PRINTS; PR00632; SONICHOG.
CC ProDom; PD003042; HH_signal; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.

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OM protein - protein search, using sw model

Run on: March 29, 2004, 18:25:24 ; Search time 45 Seconds
(without alignments)
3330.470 Million cell updates/sec

Title: US-09-883-848A-15
Perfect score: 2469
Sequence: 1 MLLARCLLLVLSLLVCS.....GMAVKSSXSRGAGGGAREGA 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-----------|--------------------|
| 1 | 2062 | 83.5 | 437 | 11 Q8C765 | Q8C765 mus musculu |
| 2 | 1544.5 | 62.6 | 434 | 13 O57404 | O57404 pleurodeles |
| 3 | 1466.5 | 59.4 | 413 | 13 Q8AXT0 | Q8axt0 fugu rubrip |
| 4 | 1454 | 58.9 | 414 | 13 Q9W7Q9 | Q9w7q9 paralichthy |
| 5 | 1308 | 53.0 | 406 | 13 Q57567 | O57567 notophthalm |
| 6 | 1262 | 51.1 | 449 | 11 Q80XI9 | Q80xi9 mus musculu |
| 7 | 1094.5 | 44.3 | 415 | 5 Q9U526 | Q9u526 branchiosto |
| 8 | 1084.5 | 43.9 | 415 | 5 O17499 | O17499 branchiosto |
| 9 | 1049.5 | 42.5 | 442 | 13 Q73803 | O73803 fugu rubrip |
| 10 | 1041.5 | 42.2 | 447 | 5 Q9GRA8 | Q9gra8 gryllus bim |
| 11 | 1010 | 40.9 | 381 | 5 Q7Z264 | Q7z264 euscorpis |
| 12 | 995 | 40.3 | 421 | 5 Q7Z263 | Q7z263 artemia san |
| 13 | 938 | 38.0 | 416 | 5 Q8MWG6 | Q8mwg6 patelia vul |
| 14 | 916 | 37.1 | 410 | 5 O61676 | O61676 lytechinus |
| 15 | 850 | 34.4 | 161 | 11 Q9R179 | Q9r179 rattus norv |
| 16 | 821 | 33.3 | 402 | 5 Q8MY56 | Q8my56 ciona intes |

| | | | | | | |
|----|-------|------|-------|----|--------|--------------------|
| 17 | 758 | 30.7 | 557 | 5 | Q8MY57 | Q8my57 ciona intes |
| 18 | 758 | 30.7 | 1073 | 5 | Q8MUM7 | Q8mum7 helobdella |
| 19 | 733 | 29.7 | 150 | 13 | Q9YGV7 | Q9ygv7 ambystoma m |
| 20 | 731 | 29.6 | 139 | 6 | Q9XSI6 | Q9xsi6 bos taurus |
| 21 | 709 | 28.7 | 138 | 13 | Q9W6C1 | Q9w6c1 eleutheroda |
| 22 | 702 | 28.4 | 177 | 11 | Q9WV29 | Q9wv29 rattus norv |
| 23 | 649 | 26.3 | 121 | 6 | Q8MJV7 | Q8mjv7 suncus muri |
| 24 | 619 | 25.1 | 185 | 5 | Q96699 | Q96699 junonia coe |
| 25 | 531 | 21.5 | 99 | 13 | Q8QGN4 | Q8qgn4 scyliorhinu |
| 26 | 526.5 | 21.3 | 202 | 6 | Q8MIN9 | Q8min9 equus cabal |
| 27 | 523 | 21.2 | 119 | 13 | O42128 | O42128 oryzias lat |
| 28 | 511 | 20.7 | 129 | 11 | Q9WUP6 | Q9wup6 rattus norv |
| 29 | 476.5 | 19.3 | 137 | 13 | O42234 | O42234 coturnix co |
| 30 | 392 | 15.9 | 80 | 13 | O42441 | O42441 oryzias lat |
| 31 | 392 | 15.9 | 87 | 5 | Q9TX30 | Q9tx30 anopheles g |
| 32 | 339 | 13.7 | 63 | 13 | Q9I8I4 | Q9i8i4 rana catesb |
| 33 | 332 | 13.4 | 64 | 13 | Q9PRF5 | Q9prf5 oryzias lat |
| 34 | 298 | 12.1 | 60 | 5 | Q95ZD8 | Q95zd8 hydra atten |
| 35 | 289 | 11.7 | 56 | 13 | Q90ZR0 | Q90zr0 oryzias lat |
| 36 | 245 | 9.9 | 74 | 6 | Q866A4 | Q866a4 sus scrofa |
| 37 | 237 | 9.6 | 49 | 5 | Q9TX33 | Q9tx33 hirudo medi |
| 38 | 229 | 9.3 | 49 | 5 | Q9TX31 | Q9tx31 tribolium c |
| 39 | 188 | 7.6 | 54 | 13 | O42233 | O42233 coturnix co |
| 40 | 187.5 | 7.6 | 125 | 11 | Q9ESH3 | Q9esh3 rattus norv |
| 41 | 175.5 | 7.1 | 48 | 5 | Q9TX32 | Q9tx32 strongyloce |
| 42 | 159.5 | 6.5 | 615 | 5 | P91573 | P91573 caenorhabdi |
| 43 | 149 | 6.0 | 1207 | 5 | Q21535 | Q21535 caenorhabdi |
| 44 | 138.5 | 5.6 | 790 | 5 | Q22872 | Q22872 caenorhabdi |
| 45 | 138.5 | 5.6 | 1137 | 5 | Q21835 | Q21835 caenorhabdi |
| 46 | 138.5 | 5.6 | 1160 | 5 | Q7YXC8 | Q7yxc8 caenorhabdi |
| 47 | 134.5 | 5.4 | 481 | 5 | O45992 | O45992 caenorhabdi |
| 48 | 126.5 | 5.1 | 1021 | 5 | Q9XUV2 | Q9xuv2 caenorhabdi |
| 49 | 123.5 | 5.0 | 2639 | 5 | O76786 | O76786 antheraea p |
| 50 | 122 | 4.9 | 702 | 6 | Q863A2 | Q863a2 canis famil |
| 51 | 121 | 4.9 | 946 | 5 | Q9XV14 | Q9xv14 caenorhabdi |
| 52 | 120.5 | 4.9 | 702 | 4 | Q7Z647 | Q7z647 homo sapien |
| 53 | 119 | 4.8 | 318 | 16 | O86703 | O86703 streptomyce |
| 54 | 119 | 4.8 | 2655 | 5 | Q964F4 | Q964f4 antheraea y |
| 55 | 118 | 4.8 | 1832 | 3 | Q8TGH8 | Q8tgh8 podospora a |
| 56 | 116 | 4.7 | 1329 | 16 | O06810 | O06810 mycobacteri |
| 57 | 116 | 4.7 | 1408 | 16 | Q8VKI7 | Q8vk17 mycobacteri |
| 58 | 115 | 4.7 | 486 | 16 | Q9AAT9 | Q9aat9 caulobacter |
| 59 | 115 | 4.7 | 795 | 16 | Q7U020 | Q7u020 mycobacteri |
| 60 | 115 | 4.7 | 1408 | 16 | Q7U022 | Q7u022 mycobacteri |
| 61 | 114.5 | 4.6 | 652 | 2 | Q44100 | Q44100 anaplasma m |
| 62 | 114 | 4.6 | 738 | 16 | Q8VKI5 | Q8vk15 mycobacteri |
| 63 | 114 | 4.6 | 741 | 16 | O06808 | O06808 mycobacteri |
| 64 | 113.5 | 4.6 | 753 | 16 | Q81IP3 | Q81ip3 bacillus ce |
| 65 | 113.5 | 4.6 | 991 | 2 | Q848A4 | Q848a4 streptomyce |
| 66 | 113.5 | 4.6 | 1318 | 5 | Q9NEI1 | Q9nei1 leishmania |
| 67 | 113.5 | 4.6 | 2172 | 2 | Q7X4R4 | Q7x4r4 streptomyce |
| 68 | 113 | 4.6 | 803 | 10 | Q7XJU6 | Q7xjj6 chlamydomon |
| 69 | 113 | 4.6 | 3324 | 2 | Q8KUF6 | Q8kuf6 actinosynne |
| 70 | 112.5 | 4.6 | 623 | 2 | Q9APG6 | Q9apg6 anaplasma m |
| 71 | 112.5 | 4.6 | 1463 | 16 | Q9ADP6 | Q9adp6 streptomyce |
| 72 | 112 | 4.5 | 513 | 6 | Q7YQC9 | Q7yqc9 canis famil |
| 73 | 112 | 4.5 | 893 | 5 | Q9W443 | Q9w443 drosophila |
| 74 | 112 | 4.5 | 912 | 5 | Q9BIT2 | Q9bit2 plectreury |
| 75 | 112 | 4.5 | 944 | 5 | Q8IRR2 | Q8irr2 drosophila |
| 76 | 111.5 | 4.5 | 209 | 2 | O849I2 | O849i2 streptomyce |
| 77 | 111.5 | 4.5 | 1016 | 5 | Q9U0V3 | Q9u0v3 leishmania |
| 78 | 111 | 4.5 | 632 | 16 | Q8CJT6 | Q8cjt6 streptomyce |
| 79 | 111 | 4.5 | 961 | 16 | Q9EWD3 | Q9ewd3 streptomyce |
| 80 | 110.5 | 4.5 | 471 | 2 | Q935Z9 | Q935z9 streptomyce |
| 81 | 110.5 | 4.5 | 624 | 16 | Q8XZA9 | Q8xxa9 ralstonia s |
| 82 | 110.5 | 4.5 | 729 | 16 | Q8P3M3 | Q8p3m3 xanthomonas |
| 83 | 110.5 | 4.5 | 1294 | 16 | O8PKH5 | O8pkh5 xanthomonas |
| 84 | 110.5 | 4.5 | 11096 | 2 | Q9L4W3 | Q9l4w3 streptomyce |
| 85 | 110 | 4.5 | 429 | 3 | Q872Y8 | Q872y8 neurospora |
| 86 | 109.5 | 4.4 | 1726 | 16 | Q7WKT6 | Q7wkt6 bordetella |
| 87 | 109.5 | 4.4 | 1729 | 16 | Q7W7E7 | Q7w7e7 bordetella |
| 88 | 109 | 4.4 | 398 | 16 | Q7WEG4 | Q7weg4 bordetella |
| 89 | 109 | 4.4 | 436 | 5 | Q967T8 | Q967t8 antheraea p |

Db 181 IHCSVKAENSVAAKSGGCFPGSSTVTLDGTTKLVKHLRSGDRVLAADDGDNPTTDFIM 240
QY 241 FLDRDDGAKKVFYVETREPRERLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FVDRDSTTRRLHYVIET-DSGQKITLTAHLLYVA--RNGTEG-----G 282
QY 301 PRALFASVRPGQRYVVAERDGR-RLLPAAVHVSITLSEEAAGAYAPLTAQGTILINRV 359
Db 283 MSVAFASQVRGQKIV---SDPERSRLPEFVTVERI-YTQEHVGSYAPVTVQGNVVVDEI 338
QY 360 LASCYAVIEEHSWAHRAFAPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPG 419
Db 339 LASCYAVIEDHDLAHWALAPVRLAHWVSSLLSRSQ-----PG 375
QY 420 AADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 376 -----GGGQKDGWHYSRLLYQVGTWLLDGHAIHPLGMSVSPS 413

RESULT 4
Q9W7Q9
ID Q9W7Q9 PRELIMINARY; PRT; 414 AA.
AC Q9W7Q9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sonic hedgehog.
GN SHH.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralicththyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99238226; PubMed=10223710;
RA Suzuki T., Ichiro O., Kurokawa T.;
RT "Retinoic acid given at late embryonic stage depresses sonic hedgehog
and Hoxd-4 expression in the pharyngeal area and induces skeletal
malformation in flounder (Paralicthys olivaceus) embryos.";
RL Dev. Growth Differ. 41:143-152(1999).
DR EMBL; AB029748; BAA82360.1; -.
DR HSSP; Q62226; 1VHH.
DR MEROPS; C46.001; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
SQ SEQUENCE 414 AA; 45945 MW; 50607BF3DB7C0DA3 CRC64;

Query Match 58.9%; Score 1454; DB 13; Length 414;
Best Local Similarity 62.4%; Pred. No. 5.6e-100;
Matches 289; Conservative 55; Mismatches 69; Indels 50; Gaps 7;
QY 1 MLLARCLLLVSSLLVCSGLACGPRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60

Db 1 MLLWTRIVLAGVICLSLVSSMGCGPGRGYGRRRHPKLTPLAYKQFIPNVAEKTIGASG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNLALAI SVMNQPGV 120
Db 61 RYEGKITRNSERFKELTPNYNTDIIFKDEENTGADRLMTQRCCKLNLALAI SVMNQPGV 120
QY 121 KLRVTEGWDEGDHSEESLHYEGRAVDITTSRDRSKYGMALARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEGDHFEESLHYEGRAVDITTSRDKSKYGTLSRLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCFPGSSTVTLDGTTKVPKALQTDGRVLAADAHGQPVYTDIFM 240
QY 241 FLDRDDGAKKVFYVETREPRERLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FIDQDSTTRRLFYVIET-DSGQKITLTAHLLFVGHNSSTERAH-----RG 285
QY 301 PRALFASVRPGQRYVVAERDGRRLLPAAVHVSITLSEEAAGAYAPLTAQGTILINRVL 360
Db 286 MSVAFASQVRPGQTVFVL---DAE-RLQPVTVKRI-YTQEHGSEFAPVTAQGTVVVDQVL 340
QY 361 ASCYAVIEEHSWAHRAFAPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
Db 341 ASCYAVIQDHELAHWALAPVRLAHWVSSLLPSSQ----- 374
QY 421 ADAPGAGATA-GIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 375 ---PQASAKDGVHWYSKILYQLGTWLLDSSHHPGLGMSVPS 414

RESULT 5
O57567
ID O57567 PRELIMINARY; PRT; 406 AA.
AC O57567;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hedgehog segment polarity homolog.
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RA Stark D.R., Gates P.B., Brockes J.P., Ferretti P.;
RT "Hedgehog homologue from Notophthalmus viridescens.";
RL Dev. Dyn. 0:0-0(1998).
CC -!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
DR EMBL; AF047466; AAC03108.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW Glycosyltransferase; Transferase.

SQ SEQUENCE 406 AA; 45072 MW; 5842CCAD5314D4D0 CRC64;

Query Match 53.0%; Score 1308; DB 13; Length 406;
Best Local Similarity 59.2%; Pred. No. 4.1e-89;
Matches 274; Conservative 41; Mismatches 80; Indels 68; Gaps 9;

QY 1 MLLARCLLLVSVLLVCSG-LACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGLGAS 59
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MKLLALPLLAACALLLGGPGLGCGPGRVIGRRPRPRLIPLSYKQFLPHVPEKTGLGAS 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 60 GRYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPG 119
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 GRYEGKIARNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPG 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 120 VKLRVTEGWDGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKA 179
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 VKLRVTEGWDGHHSEESLHYEGRAVDITTSDDRNKYGMLARLAAEAGFDWVYYESKA 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 180 HIHCSVKAENSVAKSGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFL 239
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 181 HIHCSVKSEHSAAKTGGCFPARALATLESGEKIPIADLEPGHRVLCMDEGGRRTYSDFL 240
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 240 TFLDRDDGAKKVYVIETREPRERLLTAAHLLFVA----PHNDSATGEPEASGSGPP 294
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 241 TFLDRDSTAVKEFYVETRPRLALTAHLLFVADNFTVPLTDFST----- 288
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 295 SGGALGPRLAFASVRPGQVVVVAERDGDRLRLPAAVHVSUTLSEEAAGAYAPLTAQGTI 354
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 289 -----VFASHVQPGQ--YLITE--GVLGLQPARVSVT-TQTD SGAYAPLTSHTL 334
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 355 LINRVLASCYAVIEEHSWAHRAPFRLAHALLAALAPARTDRGGDGGGGRVA 414
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 335 LVDDVVVSCFAVVQKHOLAQLAFWPLRLYHSV-----GRPE 370
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 415 LTAPGAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGM 457
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 371 -TQP-----EGHWYSLLLYRLGKVLMLMKEQHFHFGM 401
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 6
Q80XI9 PRELIMINARY; PRT; 449 AA.

AC Q80XI9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Indian hedgehog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046984; AAH46984.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hintN.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR Pfam; PF01085; HH_signal; I.
DR Pfam; PF01079; Hint; I.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; I.
DR SMART; SM00305; HintC; I.
DR SMART; SM00306; HintN; I.
DR PROSITE; PS00817; INTEIN_N_TER; I.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; I.
SQ SEQUENCE 449 AA; 49445 MW; F9ACF5B4E935E9AE CRC64;

Query Match 51.1%; Score 1262; DB 11; Length 449;
Best Local Similarity 56.9%; Pred. No. 1.2e-85;
Matches 264; Conservative 46; Mismatches 86; Indels 68; Gaps 10;

QY 7 CLLLVSVLLVCSGLACGPGRGFG-KRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGK 65
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 51 CLFLLLL--LLVPAARGCGPGRVVGSRPPRKLVP LAYKQFSPNVP EKTGLGASGRYEGK 108
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 66 ISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGVKLRVT 125
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 109 IARSSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGVKLRVT 168
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 126 EGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV 185
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 169 EGWDEDEGHSEESLHYEGRAVDITTSDDRNKYGLLARLAVEAGFDWVYYESKAHVHCSV 228
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 186 KAENSVAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLDRD 245
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 229 KSEHSAAKTGGCFPAGAQVRLNGERVALSAVKPGDRVLAMGEDGTPTFSDFLIFLDRE 288
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 246 DGAKKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASGSGPPSGALGPRLAF 305
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 289 PNRLRAFQVIETQDPPRRRLALTPAHLLFIA---DNHT-EPAAHF-----RATE 332
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 306 ASRVPRGQVVVVAERDGDRLRLPAAVHVSUTLSEEAAGAYAPLTAQGTILINRVLASCYA 365
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 333 ASHVQPGQYVLV----SGVPGLOPARVAAVS-THVALGSYAPLTHGTLVVEDVVASCF 387
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 366 VIEEHSWAHRAPFRLAHALL-AALAPARTDRGGDGGGGRVALTPGAADAP 424
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 388 AVADHHLAQLAFWPLRLFPPLAWSWTPE----- 417
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 425 GAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAG 468
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 418 -----GVHWYPQMLYRLGRLLLESTFHPPLGMS-----GAG 448
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 7
Q9U5Z6
ID Q9U5Z6 PRELIMINARY; PRT; 415 AA.
AC Q9U5Z6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog protein.
GN HEDGEHOG.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao B., Zhang Y., Zhang S., Zhang H.;
RT "A preliminary study on Qingdao amphioxus hedgehog gene.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ245882; CAB58231.2; -
DR HSSP; Q62226; 1VHH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH_signal.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHHOG.
DR PRODOM; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
SQ SEQUENCE 415 AA; 46912 MW; BF864704752BD6A8 CRC64;

Query Match 44.3%; Score 1094.5; DB 5; Length 415;
Best Local Similarity 50.2%; Pred. No. 3.3e-73;
Matches 231; Conservative 57; Mismatches 111; Indels 61; Gaps 10;

QY 3 LLARCLL-LVLVSSLLVCSG--LACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGAS 59
Db 4 VLARWMVTLVAILGTHWGPSEACGPGTRYGRRHRHPKLTFFVYKQMFVASENTFGAS 63
QY 60 GRYEGKISRNSERFELTPNYPNDIIFKDEENTGADRLMTQRCCKKLNALAISVMNQWPG 119
Db 64 GLFNGRITRDSERFHTLKQNFNTDIIFKDEEKTGADRFMTQRCCKKLNALAISVMNQWEG 123
QY 120 VKLRVTEGWEDEGHHSESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKA 179
Db 124 VKLRVTEGWEDEGHHSESLHYEGRAVDITTSRDRKTKYGMRLARLAVEAGFDWVYYESKA 183
QY 180 HIHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFL 239
Db 184 HIHCSVKAESDTTATQGGCFPEESWVTRDDGKRIRMRDVRPGDKVLSMDGAGHPVFSEVL 243
QY 240 TFLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGAL 299
Db 244 TFMDRDSRGPWVYTIKTEDRNITVTATPSHLVFVTESRDLS----- 285
QY 300 GPR-ALFASRVVRPGQRYVYVAERDGD--RRLLPAAVHVSVTLSEEAAGAYAPLTAQGTILI 356
Db 286 APRVAKFMSDVRPGE-FLLTPESDGGGFRKV---EIVSVTMREE-KGAYAPLTVHGTVVV 340
QY 357 NRVLASYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGGDRGGGGGRVALT 416
Db 341 DNVAMSCYALIESQALAHWVFAFRLYYQLTSSL----- 374
QY 417 APGAADAPGAGAT--AGIHWYSQLLYQIGTWLLDSEALHP 454
Db 375 ----WDGPSHDQTLQEGVHWYSPFFRYGISLVEPTLLHP 410

RESULT 8
O17499
ID O17499 PRELIMINARY; PRT; 415 AA.
AC O17499;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amphih protein.
GN AMPHIH.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimeid S.M.;
RT "Sequence and expression of an amphioxus hedgehog gene.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13858; CAA74169.1; -
DR HSSP; Q62226; 1VHH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHHOG.
DR PRODOM; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
SQ SEQUENCE 415 AA; 46765 MW; 5E8D2BD2158DD931 CRC64;

Query Match 43.9%; Score 1084.5; DB 5; Length 415;
Best Local Similarity 50.0%; Pred. No. 1.8e-72;
Matches 229; Conservative 53; Mismatches 119; Indels 57; Gaps 8;

QY 3 LLARCLL-LVLVSSLLVCSG--LACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGAS 59
Db 4 VLARWMVTLVAILGTHWGPSEACGPGRGFRHRHPKLTFFVYKQMFVASENTFGAS 63
QY 60 GRYEGKISRNSERFELTPNYPNDIIFKDEENTGADRLMTQRCCKKLNALAISVMNQWPG 119
Db 64 GLFNGRITRDSERFHTLKQNFNTDIIFKDEEKTGADRFMTQRCCKKLNALAISVMNQWEG 123
QY 120 VKLRVTEGWEDEGHHSESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKA 179
Db 124 VKLRVTEGWEDEGHHSESLHYEGRAVDITTSRDRKTKYGMRLARLAVEAGFDWVYYESKA 183
QY 180 HIHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFL 239
Db 184 HIHCSVKAESDTTATQGGCFSAESWVTRDDGKRIRMRDVRPGDKVLSMDSGGHPVFSEVL 243
QY 240 TFLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGAL 299
Db 244 TFMDRDSRGPWVYTIKTEDRNITVTATPSHLVFVTESRDLS----- 286
QY 300 GPR-ALFASRVVRPGQRYVYVAERDGDRLLPAAVHVSVTLSEEAAGAYAPLTAQGTILINR 358
Db 287 -PRIAKFMSDARPGEFLLTPDSGGGFR--KVIVSVTMREE-KGAYAPLTVHGTVVVDN 342
QY 359 VLASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGGDRGGGGGRVALTAP 418
Db 343 VAMSCYALIESQALAHWVFAFRLYYQLTSSL----- 374

QY 419 GAADAPGAGAT--AGIHWSQLLYQIGTWLLDSEALHP 454
Db 375 --WDGSHDQTLQEGVHWYPSFFYRIGISLVEPTLLHP 410

RESULT 9
O73803 PRELIMINARY; PRT; 442 AA.
AC O73803;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fugu hedgehog.
GN FHH.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99177347; PubMed=10077531;
RA Gellner K., Brenner S.;
RT "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu rubripes.";
RL Genome Res. 9:251-258(1999).
DR EMBL; AF056116; AAC34384.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR PRODOM; PD003042; HH signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
SQ SEQUENCE 442 AA; 49286 MW; 1CB2B423B4B748E8 CRC64;

Query Match 42.5%; Score 1049.5; DB 13; Length 442;
Best Local Similarity 48.5%; Pred. No. 8.1e-70;
Matches 224; Conservative 67; Mismatches 132; Indels 39; Gaps 9;

QY 4 LARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASGRYE 63
Db 9 LAQVSLAAWSCVWLVGQ--CGPGPGYGIRTPRKLKAMYKQFFPNLSENNLGASGRAE 66

QY 64 GKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGVKLR 123
Db 67 GKITRNSERFELVNCYNPDIVFKDEENTNADRFMTKRCCKDCLNRLALAVMNQWPGVHLR 126

QY 124 VTEGWEDEGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYYESKAHIHC 183
Db 127 VTEAWDEDEGHHPPGSLHYEGRAVDITDDRETEKYGLLAQLAVEAGFDWVYYESKYHIHC 186

QY 184 SVKAENSVAAKSGGCPGSGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLD 243
Db 187 SVKADHSVAVEKGGCFPGWSRVTVAGGFQKLSLSLTGDRVMALSETQWVFPVLLFLH 246

QY 244 RDDGAKKVFIYIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGGPPSGGALGPRA 303
Db 247 RDPESRWRFSLQTEDGR-RLAVTPHLVFSDAH-----CGPDS SQY---QA 289

QY 304 LFASRVPRGQVVVVAERDGRRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASC 363
Db 290 QFASRAQTGTCVLV--HTAGGEVHPSRIVSIT-EEESVGAYAPLTEAGSVFVDGVGLASS 345

QY 364 YAVIEEHSWAHRAFPAPFRLAHALLAALAPARTDRGDSG-----GGDRGGGGGRVA 414
Db 346 YALVEDHQLAHWAFGVPVRLSSVQLLWAEPEERSDGSKTPLPHALVRGDR-----KVC 400

QY 415 L--TAPGAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHP 454
Db 401 ARNSTSVRSEAGPRGRTSEVHWYQALLHRLGWIVLNPDLFHP 442

RESULT 10
Q9GRA8 PRELIMINARY; PRT; 447 AA.
AC Q9GRA8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hedgehog protein (Fragment).
OS Gryllus bimaculatus (two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461145; PubMed=11003837;
RA Niwa N., Inoue Y., Nozawa A., Saito M., Misumi Y., Ohuchi H.,
RA Yoshioka H., Noji S.;
RT "Correlation of diversity of leg morphology in Gryllus bimaculatus (cricket) with divergence in dpp expression pattern during leg development.";
RL Development 127:4373-4381(2000).
DR EMBL; AB044709; BAB19658.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR PRODOM; PD003042; HH signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
FT NON_TER
SQ SEQUENCE 447 AA; 48008 MW; 29AEFB061C3EE6F0 CRC64;

Query Match 42.2%; Score 1041.5; DB 5; Length 447;
Best Local Similarity 51.4%; Pred. No. 3.3e-69;
Matches 228; Conservative 47; Mismatches 118; Indels 51; Gaps 10;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 15 MPLLLRWLLLLL---LMQGAARACGPGRGAGERRASRLTPLVFKQHVNVSEHTLGAAG 71

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 72 PAERRVARDPFRFDLVPNYNADIVFKDEEGTADRLMTQRCCKLNALAI SVMNQWPGV 131

QY 121 KLRVTEGWEDEGHHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180

Db 132 RLRVIEGWEDEEGHAADSLHYEGRAVDVTTSDRRSKYCMRLARLAVEAGFDWVYETRGH 191
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKOLSPGDR-VLAADDQGRLLYSDFL 239
Db 192 IHCSVKSESSQAAKSGGCFAAESTVQ-TPGGLCALAEALRVGRGAGPGHGLAFSPVL 250
QY 240 TFLDRDDGAKKVYFVIETREPRERILLTAHLLFVAPHNDSATGEPEASSGSGPPSGAL 299
Db 251 LFLDRDP-APRTLLRVRTASGR-TLALTPSHLL-----PVARAGGE----- 290
QY 300 GPRALFASVRPGQRYVVAERDGRLLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRV 359
Db 291 -PEARFADAVRPGDALLVAADAGGAVR--PDRVLHVDAEATRGVVAPLTAAGTVVVDGV 347
QY 360 LASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTPAG 419
Db 348 LASCYAVVGGHSLAHWSFAPVRAWH-WLTANGHAAPDY----- 384
QY 420 AADAPGAGATAGIHWSQLLYQIG 443
Db 385 AHPPPPARAAPGVHWAALYSLG 408

RESULT 11
Q7Z264
ID Q7Z264 PRELIMINARY; PRT; 381 AA.
AC Q7Z264;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog (Fragment).
OS Euscorpium flavicaudis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Chactoidae; Euscorpidae; Euscorpium.
OX NCBI_TaxID=100976;
RN [1]
RP SEQUENCE FROM N.A.
RA Simonnet F., Queinnet E.;
RT "Evolution of Arthropods hedgehog gene: expression in Euscorpium
RT (Scorpiones) and Artemia (Crustacea).";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY281133; AAP38181.1; --
FT NON TER 1
SQ SEQUENCE 381 AA; 43047 MW; 0AC2196211C282B6 CRC64;

Query Match 40.9%; Score 1010; DB 5; Length 381;
Best Local Similarity 48.9%; Pred. No. 5.8e-67;
Matches 213; Conservative 54; Mismatches 99; Indels 70; Gaps 8;

QY 31 GKRRHPKLTPLAYKQFIPNVAEKTGLASGRYEGKISRNSERFKELTPNYPDIIFKDEE 90
Db 2 GRRQRPRKLTPLVFKQHPNVAETTLAASGGQKINRDETRFKELVFNYPDIIFKDEE 61
QY 91 NTGADRLMTQRCCKDLNALAISVMNQWPGVLRVTEGWDEDDGHSESLHYEGRAVDITT 150
Db 62 GTGADRLMTLRCREKLNLTALISVMNQWPGVLRVTEGWDEDDGPHAINSLHYEGRAVDITT 121
QY 151 SDRDRSKYGMRLARLAVEAGFDWVYYESKAHHCSCVKAENSVAAKSGGCFPGSATVHLEQ 210
Db 122 SDRDRSKYGMRLARLAVEAGFDWVYYESKAHHCSCVKAENSVAAKSGGCFPGSATVHLEQ 210
QY 211 GTKLVDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGAKKVYFVIETREPRERLLTAAH 270
Db 181 GAKMSELDVGNELDCSRNGFTYSQVIMFLDWDPKTNRQFYVLTHTNTRS-ITLTPSH 239
QY 271 LFLVAPHNDSATGEPEASSGSGPPSGALGPRALFASVRPGQRYVVAERDGRRLP 330
Db 240 LIFVVGNGKT-----RVVTRDVRPGH--YILAKHPRENVTSP 276
QY 331 AVHVSRTLSEEAAGAYAPLTAQGTILINRVLASCYAVIEHSHWAHRAFPRLAHA----- 385
Db 277 LVTHVT-TIVTTGVYAPLTIQGNLWVDGFWASCYAVINDQTMHAWFLPVRVADSVKEMV 335

QY 386 -----LLAALAPARTDRGGDSGGDRGGGGRVALTPGAADAPGAGATAGIHWSQ 437
Db 336 FRILEKPHLMERTSPSRR-----AP-----DPGIHMYAR 364
QY 438 LLYQIGTWLSDSEALH 453
Db 365 SLYFIARYVLPSSYLX 380

RESULT 12
Q7Z263
ID Q7Z263 PRELIMINARY; PRT; 421 AA.
AC Q7Z263;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog (Fragment).
OS Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_TaxID=6661;
RN [1]
RP SEQUENCE FROM N.A.
RA Simonnet F., Queinnet E.;
RT "Evolution of Arthropods hedgehog gene: expression in Euscorpium
RT (Scorpiones) and Artemia (Crustacea).";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY281134; AAP38182.1; --
FT NON TER 1
SQ SEQUENCE 421 AA; 47289 MW; 350B034CFD72817A CRC64;

Query Match 40.3%; Score 995; DB 5; Length 421;
Best Local Similarity 49.0%; Pred. No. 8.7e-66;
Matches 223; Conservative 53; Mismatches 103; Indels 76; Gaps 11;

QY 31 GKRRHPKLTPLAYKQFIPNVAEKTGLASGRYEGKISRNSERFKELTPNYPDIIFKDEE 90
Db 2 GRRRGPRKLTPLVFKQHPNMSENTLGLASGLSEGITRDDPRFKDLVFNYSDIIFKDEE 61
QY 91 NTGADRLMTQRCCKDLNALAISVMNQWPGVLRVTEGWDEDDGHSESLHYEGRAVDITT 150
Db 62 GTGADRLMTQRCCKELNLTALISVMNQWPGVLRVTEGWDEDDGHASNSLHYEGRAVDITT 121
QY 151 SDRDRSKYGMRLARLAVEAGFDWVYYESKAHHCSCVKAENSVAAKSGGCFPGSATVHLEQ 210
Db 122 SDRDRSKYGMRLARLAVEAGFDWVYYESRAHHTSVKSESSAARSGGCTGDSLVTLDG 181
QY 211 GTKLVDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGAKKVYFVIETREPRERLLTAAH 270
Db 182 EQVKMSDVRIGDRVLAVDEDNLIYSEVLLFLDRDVTNRQFVKL-TTESGETVELTASH 240
QY 271 LFLVAPHN-----DSATGE---PEASSGSGPPSGALGPRALFASVRPGQ 313
Db 241 LIFTVQSNYEYETMAKLENNENIDSSIEENEITELSDNEGD-----LFVSKL---Q 287
QY 314 RVYVVAER-----DGRRLLPAAVHVSRTL---SEEA---AGAYAPLTAQGTILINRVL 360
Db 288 FHTLVAETFAKNVKG DYLLVKNKVGKLVQLVTEVAFSVQTVGYAPLNTGTIIIVNSVA 347
QY 361 ASCYAVIEHSHWAHRAFP-----FRLAHALLAALAPARTDRGGDSGGDRGGGGRVA 414
Db 348 ALLYAVVDVSHLIAHWAFFPLRWYSNFNEAYSILSYARLK-DKNSRTKFE----- 397
QY 415 LTAPGAADAPGAGATAGIHWSQLLYQIGTWLSDS 449
Db 398 -----GIHWYAKLLYDLDSHYIVPS 416

RESULT 13
Q8MWG6
ID Q8MWG6 PRELIMINARY; PRT; 416 AA.
AC Q8MWG6;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog.
GN HH.
OS Patella vulgata (Common limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Eogastropoda; Docoglossa;
OC Patellina; Patelloidea; Patellicidae; Patella.
OX NCBI_TaxID=6465;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22070397; PubMed=12075342;
RA Nederbragt A.J., Van Loon A.E., Dictus W.J.;
RT "Evolutionary biology: Hedgehog crosses the snail's midline."
RL Nature 417:811-812(2002).
DR EMBL; AF435840; AAM50752.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR PRODOM; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
SQ SEQUENCE 416 AA; 45975 MW; 21A22CD695956780 CRC64;

Query Match 38.0%; Score 938; DB 5; Length 416;
Best Local Similarity 42.5%; Pred. No. 1.5e-61;
Matches 192; Conservative 82; Mismatches 118; Indels 60; Gaps 8;

QY 9 LLVLVSSLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGLGASGRYEGKISR 68
Db 16 IILFITSLT---HACGPGRGSGRRKAKKHTPLVFKQNPVNSENSLGASGMSEGRIKR 71

QY 69 NSERFKELTNPYNPDIIIFKDEENTGADRLMTQRCQKLNALAI SVMNQWPGVKLRVTEGW 128
Db 72 DDAKFKDLVRNHNADIVFKNEEGDGSVHMTRRCQDKNLSLAVSMNWKGVMLRVTEAW 131

QY 129 DEDGHHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYVESKAHIHCSVKAE 188
Db 132 NDNNSHAKDSLHYEGRAVDITTSKDRAKYGMRLARLAVEAGFDWVYVESRGIHCSVKSD 191

QY 189 NSVAAKSGGCGFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGA 248
Db 192 SSVAIKIGGCGFGTGVLTQET-GWKTMSQVVAGDSVLSMNSNGKLEYSPIAFIDRNERE 250

QY 249 KKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALFASR 308
Db 251 LERYITLHT-EDKKDITLTSKHLIYMSNSTVTTDDVTDSFN-----VVYADD 296

QY 309 VRPGQVVVVAERDGD---RRLLPAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCY 364
Db 297 VIEGDYLVLTSDPVGVEIKPTRVLTISEHTI-----QGVAPLTLNGNIVDGVVVSVCY 350

QY 365 AVIEEHSWAHRAPFRLAHAL---LAALAPARTDRGDSGGGGRGGGRVALTAPGAA 421
Db 351 AVVSNANLAHVVPAPVRGLHLVLSQYVPWLAPSTHHQNFTQN----- 391

QY 422 DAPGAGATAGIHWYSQLLYQIGTWLLDSEALH 453
Db 392 -----GVRWYAKLLYNIGSTFLSAETLH 414

RESULT 14
O61676 PRELIMINARY; PRT; 410 AA.
AC O61676;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RA Hertzler P.L., McClay D.R.;
RT "A sea urchin hedgehog homolog."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059606; AAC15065.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR PRODOM; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
SQ SEQUENCE 410 AA; 46071 MW; 875CF889DA6FDBED CRC64;

Query Match 37.1%; Score 916; DB 5; Length 410;
Best Local Similarity 45.5%; Pred. No. 6.4e-60;
Matches 206; Conservative 65; Mismatches 128; Indels 54; Gaps 11;

QY 4 LARCLLLVLVSSL-LVCSGLACGPGRGFGKRRH-PKLTPLAYKQFIPNVAEKTGLGASGR 61
Db 6 MVKWLTVQITTALCLIALTQACHPGRS-CKTSHRPRNRTPLQYKQKVPNISEDTFGASGP 64

QY 62 YEGKISRNSERFKELTNPYNPDIIIFKDEENTGADRLMTQRCQKLNALAI SVMNQWPGVK 121
Db 65 PEGRIDRDDERFSKLSPNNDIIVFKDEEGTGADRLMTQRCQKLNLTALISVMNEWPGIK 124

QY 122 LRVTEGWEDEGHHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYVESKAHI 181
Db 125 LRVWEAWDED-QPNVEPLHAEGRAVDITTSDDRDKNKGALARLAVEAGFDWVSYESKAWV 183

QY 182 HCSVKAENSVAAKSGGCGFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTF 241
Db 184 HCSVKSESAAKNSGGCGFGFSQAYLKNGRMISMLDIRVGDEVAVNNNGELDYSDVIMI 243

QY 242 LDRDDGAKKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGP 301
Db 244 VHRKLNDSITLFVIET-EDKTIVQLTPQHLLIYVS-----ERESNFDQS----- 285

QY 302 RALFASRVPRGQVVVVAERDGDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLA 361
Db 286 RAVFASEVRTNQFYTTAQ-NHDRGVRPMKVSVT-TRLGHTAVAPVTRQGSLSVIDGVAV 343

QY 362 SCYAVIEEHSWAHRAPFRLAHALLAALAPARTDRGDSGGGGRGGGRVALTAPGAA 421
Db 344 SSYAVMRDEWVAHASFAPIRWYTYISHMLGITDITDTGQEQ----- 383

OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22126614; PubMed=12128232;
RA Takatori N., Satou Y., Satoh N.;
RT "Expression of hedgehog genes in Ciona intestinalis embryos.";
RL Mech. Dev. 116:235-238 (2002).
DR EMBL; AB078508; BAC06180.1; -
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog hintC.
DR InterPro; IPR003587; Hedgehog hint_N.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR TIGRFAMs; TIGR01445; intein_Nterm; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00817; INTEIN_NTER; 1.
SQ SEQUENCE 557 AA; 61455 MW; A81FD95B77B76DE3 CRC64;

Query Match 30.7%; Score 758; DB 5; Length 557;
Best Local Similarity 41.7%; Pred. No. 5.8e-48;
Matches 186; Conservative 63; Mismatches 155; Indels 42; Gaps 12;
QY 23 ACGPGRGFGKRRHP-KKLTPLAYKQFIPNVAEKTLGASGRYEGKISRNSERFK-ELTPNY 80
Db 129 ACRPGHSGGSRMPGRELVFLKGEYVPMSEQTIGASGPVTGRIRADTPRFRQELVPNW 188
QY 81 NPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGVKLRVTEGWDGHHSESLH 140
Db 189 NTDIEFRDEESNEDRFMTPICRARLDYLAILVANQWARVKKVLEAWDDGNDKANDPLH 248
QY 141 YEGRVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHHCYKAEKSVAAKSGGCFP 200
Db 249 YEGRVDITTDADRKNKYPILARLAVAGFDWVKYDGKV-VHCSVKSESDAAKYGGCFP 307
QY 201 GSATVHLEQGGTKLVKDLSPGDRVLADDDQGRLLYSDFLTFLD-RDD---GAKKVFFYVIE 256
Db 308 GESTVIVPGEHVPMSSLOPGDQVLADKSGAVITDTFLSFMARSDIVSGHQAYRQMV 367
QY 257 -TREPRERLLTAAHLLFVA-PHNDSATCEPEASSGSGPPSGGALG-----PRALFASR 308
Db 368 ITTENGFSVTLTRNHLIYVSKPTYDASL--LTATSNATQONNERLGLQDFTSPHSSFAAK 425
QY 309 VRPGQRVVVAER-----DGDRLLLPAAVHVSVTLSSEEAGAYAPLTAQGTILINRVLASC 363
Db 426 VRQGDYIYTLNPSHTGPDTPSATVRPSRVVSVRTIETASGAYAPLTYSGTIIVGTTAASC 485
QY 364 YAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDGGGGRGGRVALTPGAADA 423
Db 486 YAVIESDVIAHTVVSPPFRYYHWLSLWF-----NGDSKDHNRNCTHVGPVR----- 529
QY 424 PGAGATAGIHWYSQLLYQIGTWLLDS 449
Db 530 ----PTDGISLYSKLHQIFSKVLPS 551

RESULT 18
Q8MUM7
ID Q8MUM7 PRELIMINARY; PRT; 1073 AA.
AC Q8MUM7;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog-like protein.
GN HH.
OS Helobdella robusta (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Helobdella.
OX NCBI_TaxID=6412;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang D., Huang F., Li D., Shankland M., Gaffield W., Weisblat D.A.;
RT "A hedgehog homolog regulates gut formation in leech (Helobdella).";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF517943; AAM70491.1; -
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
SQ SEQUENCE 1073 AA; 122877 MW; 08859088DF387062 CRC64;

Query Match 30.7%; Score 758; DB 5; Length 1073;
Best Local Similarity 31.6%; Pred. No. 1.5e-47;
Matches 180; Conservative 69; Mismatches 142; Indels 178; Gaps 10;
QY 11 VLVSSLLVCSGL---ACGPGRG-FGKRRHPKLTPLAYKQFIPNVAEKTLGASGRYEGK 65
Db 193 VLIFFLVVFDGRCFVSGCGPGRSYFSPKGRKMTFFVLKQHVNLSETTLGASGQPEGK 252
QY 66 ISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGVKLRVT 125
Db 253 VSRGDPEFKLVTKNPNIIIFQNSEGTGADRVMSKRCSDKLNALSLTMEQWPGVRLRV 312
QY 126 EGWDEDGHHSESLHYEGRVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHHCYV 185
Db 313 EAWDEDETHPEDSLHYEGRVDITTSDDKSKYGMLARLAVEAGFDWVHYEYRSHHCYV 372
QY 186 KAENSVAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAD-----DQGRLLYSDFLTFLDRD- 245
Db 373 KSDSLIAEHAGGCFPEATLYRPDWSAVSMRDLQIGDLVWTFDGDVIKTPPPFLSLRWP 432
QY 229 -----DQGRLLYSDFLTFLDRD- 245
Db 433 PWLLKLLQWPLLLSSSSPSRSSFHSLSSSSSSSSSSSSSSSSSSSSSLSAGRLVLTETVIAFLHKDP 492
QY 246 -----DGAKKVFFYVIETREPRER----- 263
Db 493 NLEMEFVEVKVGNLNDNDDGNDNDDSGFDYDNHYHLLHSRQQQKQFQQQQQQQQQQ 552
QY 264 -----LLLTAAHLLFVAPH-----NDSATGEPEASSGSG----- 292
Db 553 QQQQHHHLITLTDNHLIFLNRHHHHYQHHHHFKMKKKPNDDDSRHSIDESDKNDGVSV 612
QY 293 -----PPSGGALGPALFASRVPRPGQRVVVAER 321
Db 613 NDDYNSDKSNIITSFAAYLNTANDFLFIVTPPPSSSPTPTQPPPPSSSTPPSTSSSSTSSH 672
QY 322 ----DGDRLLLPAAVHVSVTLSSEEAGAYAPLTAQGTILINRVLASCYAVIEHSHWAHRA 377
Db 673 HLTSSDTTIVEPTKIIVGISKTRH-RGIYAPLTHGTMLVNGIWSYATYNNHHLAHMSL 731
QY 378 APFR----LAHALAALAPARTDRGGDSG 402
Db 732 APLRWLSVAGVVKGAVGTALEVVGGFAG 760

RESULT 19
Q9YGV7
ID Q9YGV7 PRELIMINARY; PRT; 150 AA.
AC Q9YGV7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sonic hedgehog (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Torok M.A., Izpizua-Belmonte J.C., Gardiner D.M., Bryant S.V.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031480; AAD18128.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16599 MW; 986F65037A69A8AC CRC64;

Query Match 29.7%; Score 733; DB 13; Length 150;
Best Local Similarity 93.3%; Pred. No. 6.6e-47;
Matches 140; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 83 DIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGVKLRVTEGDEGHSESLHYE 142
DB 1 DIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGVKLRVTEGDEGHSESLHYE 60

QY 143 GRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYVESKAHHC SVKAENSVAAKSGGCFPGS 202
DB 61 GRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYVESKAHHC SVKAENSVAAKSGGCFPAS 120

QY 203 ATVHLEGGGKLVKOLSPGDRVLAADDQGR 232
DB 121 AKVTLEHGVTTPVKOLRPGDRVLAADQGR 150

RESULT 20
Q9XS16
ID Q9XS16 PRELIMINARY; PRT; 139 AA.
AC Q9XS16;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sonic hedgehog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tooth germ;
RA Koyama E., Iwamoto M., Ohmori T., Kurisu K., Wu C., Ookura T.,
RA Bashir M.M., Tucker T., Pacifici M.;
RT "Development of Stratum Intermedium and its Role as a Sonic Hedgehog-
Signaling Structure During Odontogenesis.";

Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF144100; AAD33926.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 139
SQ SEQUENCE 139 AA; 15961 MW; C83B0B96982046B1 CRC64;

Query Match 29.6%; Score 731; DB 6; Length 139;
Best Local Similarity 98.6%; Pred. No. 8.3e-47;
Matches 137; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 43 AYKQFIPNVAEKTILGASGRYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRC 102
DB 1 AYKQFIPNVAEKTILGASGRYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRC 60

QY 103 KDKLNALAI SVMNQPGVKLRVTEGDEGHSESLHYE GRAVDITTSDDRDRSKYGMRLA 162
DB 61 KDKLNALAI SVMNQPGVKLRVTEGDEGHSESLHYE GRAVDITTSDDRDRSKYGMRLA 120

QY 163 RLAVEAGFDWVYVESKAHI 181
DB 121 RLAVEAGFDWVYVESKAHI 139

RESULT 21
Q9W6C1
ID Q9W6C1 PRELIMINARY; PRT; 138 AA.
AC Q9W6C1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sonic hedgehog protein (Fragment).
GN SHH1.
OS Eleutherodactylus coqui (Puerto Rican coqui).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;
OC Telmatobiinae; Eleutherodactylus.
OX NCBI_TaxID=57060;
RN [1]
RP SEQUENCE FROM N.A.
RA Carl T.F., Richardson M.K., Olsson L., Schlosser G., Klymkowsky M.W.,
RA Hanken J.;
RT "Differences in vertebrate limb development revealed by studies of the
direct developing frog E. coqui.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113403; AAD23436.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15751 MW; FF4156A17F4681F0 CRC64;

Query Match 28.7%; Score 709; DB 13; Length 138;
Best Local Similarity 96.4%; Pred. No. 3.6e-45;
Matches 133; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 48 IPNVAEKTILGASGRYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKDLN 107

Db 1 IPNVAEKTGLGASGRYEGKITRNSERFKELTPNYSNDIIFKDEENTAADRLMTQRCCKDLN 60

QY 108 ALAISVMNQWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVE 167

Db 61 ALAISVMNLWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVE 120

QY 168 AGFDWVYVESKAHIHCSV 185

Db 121 AGFDWVYVESKAHIHCSV 138

RESULT 22

Q9WV29 PRELIMINARY; PRT; 177 AA.

AC Q9WV29

DT 01-NOV-1999 (TReMBLrel. 12, Created)

DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Indian hedgehog protein (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Kidney;

RA Garges P.L., Meyer R.A. Jr., Brown C.A., Price D.K.;

RT "Indian hedgehog in rat.;"

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162914; AAD45372.1; -.

DR HSSP; Q62226; 1VHH.

DR MEROPS; C46.003; -.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0007267; P:cell-cell signaling; IEA.

DR GO; GO:0007275; P:development; IEA.

DR GO; GO:0016539; P:protein splicing; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR009045; Hedgehog/DD_pept.

DR InterPro; IPR003587; Hedgehog_hint_N.

DR InterPro; IPR006141; Intein_S.

DR InterPro; IPR001657; Peptidase C46.

DR InterPro; IPR001767; Pept_C46_hint.

DR Pfam; PF01085; HH_signal; 1.

DR Pfam; PF01079; Hint; 1.

DR PRINTS; PR00632; SONICHOG.

DR ProDom; PD003042; HH_signal; 1.

DR SMART; SM00306; HintN; 1.

DR PROSITE; PS50817; INTEIN_N_TER; 1.

FT NON_TER 1

FT NON_TER 177

SQ SEQUENCE 177 AA; 19739 MW; CA5871626A565F65 CRC64;

Query Match 28.4%; Score 702; DB 11; Length 177;

Best Local Similarity 74.0%; Pred. No. 1.7e-44;

Matches 131; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 97 LMTQRCCKDLNALAISVMNQWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRS 156

Db 1 LMTQRCCKDLNSLAISVMNQWPGVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRN 60

QY 157 KYGMLARLAVEAGFDWVYVESKAHIHCSVKAENSVAKSGGCFGSATVHLEQGCKLVK 216

Db 61 KYGLLARLAVEAGFDWVYVESKAHVCHSVKSEHSAAKTGGCFPAGAQVHLETGERVALS 120

QY 217 DLSPGDRVLAADQGRLLYSDFLTFLDRDDCAKKVFIETREPRERLLTAHLLF 273

Db 121 AVKPGDRVLAMGEDGNFTFSDVLIFLDREPRLRAFOVIETQDPPRRLALTPAHLF 177

RESULT 23

Q8MJV7 PRELIMINARY; PRT; 121 AA.

ID Q8MJV7

AC Q8MJV7;

DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Sonic hedgehog (Fragment).

GN SSHH.

OS Suncus murinus (House shrew) (Musk shrew).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.

OX NCBI_TaxID=9378;

RN [1]

RP SEQUENCE FROM N.A.

RA Ogi H., Tabata M.J., Yamanaka A., Yasui K., Uemura M.;

RT "COMPARISON OF EXPRESSION PATTERNS OF FIBROBLAST GROWTH FACTOR 8, BONE MORPHOGENETIC PROTEIN 4 AND SONIC HEDGEHOG IN JAW DEVELOPMENT OF THE HOUSE SHREW, SUNCUS MURINUS.;"

RL Cell. Mol. Biol. 48:OL289-OL296 (2002).

DR EMBL; AB081406; BAC02893.1; -.

DR GO; GO:0007267; P:cell-cell signaling; IEA.

DR GO; GO:0007275; P:development; IEA.

DR InterPro; IPR009045; Hedgehog/DD_pept.

DR InterPro; IPR000320; HH_signal.

DR InterPro; IPR001657; Peptidase_C46.

DR Pfam; PF01085; HH_signal; 1.

DR PRINTS; PR00632; SONICHOG.

DR ProDom; PD003042; HH_signal; 1.

FT NON_TER 1

FT NON_TER 121

SQ SEQUENCE 121 AA; 13919 MW; D159C4C5DA5AEA16 CRC64;

Query Match 26.3%; Score 649; DB 6; Length 121;

Best Local Similarity 99.2%; Pred. No. 8.7e-41;

Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 71 ERFKELTPNYPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGWDE 130

Db 1 ERFKELTPNYPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGVKLRVTEGWDE 60

QY 131 DGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHIHCSVKAENS 190

Db 61 DGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHVCHSVKAENS 120

QY 191 V 191

Db 121 V 121

RESULT 24

O96699 PRELIMINARY; PRT; 185 AA.

ID O96699

AC O96699;

DT 01-MAY-1999 (TReMBLrel. 10, Created)

DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Hedgehog protein (Fragment).

GN HH.

OS Junonia coenia (Peacock butterfly) (Precis coenia).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.

OX NCBI_TaxID=39708;

RN [1]

RP SEQUENCE FROM N.A.

RA Keys D.N., Lewis D.L., Selegue J.E., Pearson B.J., Goodrich L.V., Johnson R.L., Gates J., Scott M.P., Carroll S.B.;

RT "Recruitment of a hedgehog regulatory circuit in butterfly eyespot evolution.;"

RL Science 0:0-0 (1999).

DR EMBL; AF117742; AAD08931.1; -.

DR HSSP; Q62226; 1VHH.

DR GO; GO:0007267; P:cell-cell signaling; IEA.

DR GO; GO:0007275; P:development; IEA.

DR InterPro; IPR009045; Hedgehog/DD_pept.

DR InterPro; IPR000320; HH signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1 185
FT NON_TER 185
SQ SEQUENCE 185 AA; 20745 MW; E9B9F4CE2FAAE662 CRC64;

Query Match 25.1%; Score 619; DB 5; Length 185;
Best Local Similarity 68.2%; Pred. No. 2.7e-38;
Matches 116; Conservative 21; Mismatches 31; Indels 2; Gaps 2;

QY 58 ASGRYEGKISRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQW 117
Db 3 ASGPPEGRITRDDEKFRDLVFNYPDIDFKDDEGTGADRLMTQRCCKELNTLAISVMNQW 62

QY 118 PGVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVES 177
Db 63 PGVLRVIEGWDEENSHLDSLHYEGRAVDLTTSDDHSGKNGMLARLAVEAGFDWVYFEN 122

QY 178 KAHIHCSVKAENSVAAKSGGPPGSATVHLEQGQTKLVKDLSPGDRVLAA 227
Db 123 RSYIHCSVKTESSVGT-GAGCFPPSGAVVHTENGPPXD-IASLKKGNKVLAA 170

RESULT 25
Q8QGN4
ID Q8QGN4 PRELIMINARY; PRT; 99 AA.
AC Q8QGN4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sonic hedgehog (Fragment).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21930458; PubMed=11932743;
RX Tanaka M., Munsterberg A., Anderson W.G., Prescott A.R., Hazon N.,
RA Tickle C.;
RT "Fin development in a cartilaginous fish and the origin of vertebrate
limbs";
RL Nature 416:527-531(2002).
DR EMBL; AF393835; AAM08228.1;
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1 99
FT NON_TER 99
SQ SEQUENCE 99 AA; 11468 MW; 831864BDB34A1A20 CRC64;

Query Match 21.5%; Score 531; DB 13; Length 99;
Best Local Similarity 98.0%; Pred. No. 4e-32;
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 78 PNYNPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGVKLRVTEGWDEDDGHSEEE 137
Db 1 PNYNPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGVKLRVTEGWDEDDGHSEEE 60

QY 138 SLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVE 176
Db 61 SLHYEGRAVDITTSDDRTKYGMLARLAVEAGFDWVYVE 99

RESULT 26
Q8MIN9
ID Q8MIN9 PRELIMINARY; PRT; 202 AA.
AC Q8MIN9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Indian hedgehog (Fragment).
GN IHH.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RN SEQUENCE FROM N.A.
RP Semevolos S.A., Nixon A.J.;
RT "Partial nucleotide sequence for equine Indian hedgehog mRNA";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY112896; AAM44071.1;
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001657; Peptidase_C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR InterPro; IPR002375; Pr/py_py_transf.
DR Pfam; PF01085; HH signal; 1.
DR Pfam; PF01079; Hint; 1.

DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
FT NON_TER 1 202
FT NON_TER 202
SQ SEQUENCE 202 AA; 21601 MW; 3C9E2872BD3E6FID CRC64;

Query Match 21.3%; Score 526.5; DB 6; Length 202;
Best Local Similarity 51.1%; Pred. No. 2.4e-31;
Matches 114; Conservative 28; Mismatches 60; Indels 21; Gaps 4;

QY 155 RSKYGMRLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCPFGSATVHLEQGQTKL 214
Db 1 RNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAAKTGCFPAGAQVRLESGARVA 60

QY 215 VKDLSPGDRVLAAADQGRLLYSDFLTFLDRDDGAKKVFYVVIETREPRERLLLTAAHLLFV 274
Db 61 LSAVRPGDRVLAMGEDGNPTFSDVLIFLDREPDRRLRAFQVIETQDPPRRLALTPAHLFT 120

QY 275 APHNDSATGEPEASSGSGPPSGGALGPRALFASRVPRGQVYVVAERDGDRLLPAAVHS 334
Db 121 ANNH-----SEFAAHF-----RATFASQVQPGQYVLA----GVPGLPARVAA 160

QY 335 VTLSEEAAGAYAPLTAQGTILINRVLASCYAVIEEHSWAHRAF 377
Db 161 VS-THVALGAYAPLTRHGTLLVVEDVVVASCFAAVADHHLAQLAF 202

RESULT 27
O42128
ID O42128 PRELIMINARY; PRT; 119 AA.
AC O42128;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Shh (Fragment).

GN ME-SHH.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=bbrr; TISSUE=Embryo;
RA Araki K.;
RT "The analysis of medaka haploid development.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB007129; BAA22368.1; -.
DR HSSP; Q62226; 1VHH.
DR MEROPS; C46.001; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 119
FT SEQUENCE 119 AA; 13179 MW; A4868AC2E475CB1B CRC64;

Query Match 21.2%; Score 523; DB 13; Length 119;
Best Local Similarity 82.4%; Pred. No. 2.1e-31;
Matches 98; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 123 RVTEGWDEGHSEESLHYEGRAVDITTSRDRSKYGLARLAVEAGFDWVYYESKAH 182
Db 1 RVTEGWDEGHFEESLHYEGRAVDITTSRDRSKYGLRLAVEAGFDWVYYESKAH 60

QY 183 CSVKAENSVAKSGGCPGSGATVHLEQGGTKLVKDLSPGDRVLADDDQGRLLYSDFLT 241
Db 61 CSVKAESSVAKSGGCPGSGSTVLENGTQRPVKQLQPGDRVLADYDGNPNVYTFIMF 119

RESULT 28
Q9WUP6 PRELIMINARY; PRT; 129 AA.
ID Q9WUP6;
AC Q9WUP6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Desert hedgehog protein (Fragment).
GN DHH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Garges P.L.; Meyer R.A. Jr.; Brown C.A.; Price D.K.;
RT "Desert hedgehog in the rat."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF148226; AAD31927.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.

DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 129
SQ SEQUENCE 129 AA; 14578 MW; AB33509B3E751319 CRC64;

Query Match 20.7%; Score 511; DB 11; Length 129;
Best Local Similarity 71.4%; Pred. No. 1.8e-30;
Matches 90; Conservative 24; Mismatches 10; Indels 2; Gaps 2;

QY 23 ACGPGRG-FGKRHPKK-LTPLAYKQFIPNVAEKTLGASGRYEGKISRNSERFKELTPNY 80
Db 4 SCGPGRGPVGRRRYVRKQLVPLLYKQFVPSMPERTLGASGPAEGRVTRGSEFRDLVPNY 63

QY 81 NPDIIFKDEENTGADRLMTQRCCKLNLALAISVMNQWPGVKLRVTEGWDEDEGHSEESLH 140
Db 64 NPDIIFKDEENSGADRLMTQRCCKERNALAIAMNMWPGVRLRVTEGWDEDEGHHAQDSLH 123

QY 141 YEGRV 146
Db 124 YEGRAL 129

RESULT 29
O42234 PRELIMINARY; PRT; 137 AA.
ID O42234;
AC O42234;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sonic hedgehog (Fragment).
GN SHH.
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98167903; PubMed=9435297;
RA Borycki A.G.; Mendham L.; Emerson C.P. Jr.;
RT "Control of somite patterning by Sonic hedgehog and its downstream
RT signal response genes."
RL Development 125:777-790(1998).
DR EMBL; AF022882; AAB80949.1; -.
DR MEROPS; C46.002; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003586; Hedgehog hintC.
DR InterPro; IPR001657; Peptidase C46.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR SMART; SM00305; HintC; 1.
FT NON_TER 1
FT SEQUENCE 137 AA; 14571 MW; 7FD29DF815AF1532 CRC64;

Query Match 19.3%; Score 476.5; DB 13; Length 137;
Best Local Similarity 60.2%; Pred. No. 7.3e-28;
Matches 103; Conservative 12; Mismatches 21; Indels 35; Gaps 5;

QY 293 PPSGALGPRLAFASRVPQGVVVAERDGRLLPAAVSHSVTLSEEAAGAYAPLTAQG 352
Db 1 PTSG-----QAFFASNVKPGQVYVLGE--GGRQLLPASVHSVSLREEASGAYAPLTAQG 53

QY 353 TILINRVLASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGGSDGGDRGGGGR 412
Db 54 TILINRVLTSCYAVIEEHSWAHWAFAFRLAQGLLAALCP----- 93

QY 413 VALTAPGAADAPGAG-ATAGIHWYSQLLYQIGTWLDDSEALHPLGMVAVKSS 462
Db 94 -----DGA--IPFAGTTTIGIHWYSRLLYHIGSWVLDDGDALHPLGMVAVAS 137

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RESULT 30
O42441
ID O42441 PRELIMINARY; PRT; 80 AA.
AC O42441;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sonic hedgehog (Fragment).
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Koester R., Stick R., Loosli F., Wittbrodt J.;
RT "Medaka spalt acts as a target gene of hedgehog signaling.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97019; CAB09695.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 9180 MW; 5E18295E6E05A4D7 CRC64;

Query Match 15.9%; Score 392; DB 13; Length 80;
Best Local Similarity 91.2%; Pred. No. 6.7e-22;
Matches 73; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 88 DEENTGADRLMTQRCXKLNALAISVMNQPGVKLRVTEGWDEDDGHSESLHYEGRAVD 147
Db 1 DEENTGADRLMTQRCXKLNLSAISVINQPGVKLRVTEGWDEDDGHSESLHYEGRAVD 60

QY 148 ITTSDRRSKYGMRLARLAVE 167
Db 61 ITTSDRRSKYGTLSRLAVE 80

RESULT 31
Q9TX30
ID Q9TX30 PRELIMINARY; PRT; 87 AA.
AC Q9TX30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog HH protein homolog (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OC NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, genetic linkage and limb patterning activity of a murine
RT hedgehog gene.";
RL Development 120:3339-3353(1994).
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
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DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 87
SQ SEQUENCE 87 AA; 10017 MW; 0590DB14605D13CE CRC64;

Query Match 15.9%; Score 392; DB 5; Length 87;
Best Local Similarity 80.5%; Pred. No. 7.5e-22;
Matches 70; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 101 RCKDKLNALISVMNQPGVKLRVTEGWDEDDGHSESLHYEGRAVDITTSDRRSKYGM 160
Db 1 RCKEKLNILAVSMNQPGVLRVTEGWDEDDHMHAPESLHYEGRAVDIMTSDKORSKIGM 60

QY 161 LARLAVEAGFDWVYVESKAHIHCSVKA 187
Db 61 LARLAVEAGFDWVYVESRSHIHCSVKS 87

RESULT 32
Q9I8I4
ID Q9I8I4 PRELIMINARY; PRT; 63 AA.
AC Q9I8I4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sonic hedgehog (Fragment).
GN SHH.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OC NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Wroblewski E.E., Patterson J.M.;
RT "Cloning of sonic hedgehog from the bullfrog Rana catesbeiana.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275308; AAF89204.1; -.
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 63
SQ SEQUENCE 63 AA; 7227 MW; 4C1FC3BD7D6F4B13 CRC64;

Query Match 13.7%; Score 339; DB 13; Length 63;
Best Local Similarity 96.8%; Pred. No. 4.2e-18;
Matches 61; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 125 TEGWDEDDGHSESLHYEGRAVDITTSDRRSKYGMRLARLAVEAGFDWVYVESKAHIHCS 184
Db 1 TEGWDEDDGHSDLSLHYEGRAVDITTSDRRNKYGMRLARLAVEAGFDWVYVESKAHIHCS 60

QY 185 VKA 187
Db 61 VKA 63

RESULT 33
Q9PRF5
ID Q9PRF5 PRELIMINARY; PRT; 64 AA.
AC Q9PRF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE SONIC hedgehog (Fragment).
GN SHH.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA, and HNI;
RX MEDLINE=20082974; PubMed=10613850;
RA Ohtsuka M., Makino S., Yoda K., Wada H., Naruse K., Mitani H.,
RA Shima A., Ozato K., Kimura M., Inoko H.;
RT "Construction of a linkage map of the Medaka (Oryzias latipes) and
RT mapping of the Da mutant locus defective in dorsoventral patterning.";
RL Genome Res. 9:1277-1287(1999).
DR EMBL; AB030474; BAA85141.1; -;
DR EMBL; AB030473; BAA85140.1; -;
DR HSSP; Q62226; 1VHH.
DR MEROPS; C46.001; -;
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH signal; 1.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 64
SQ SEQUENCE 64 AA; 7420 MW; 3D4798E98D741F08 CRC64;

Query Match 13.4%; Score 332; DB 13; Length 64;
Best Local Similarity 93.8%; Pred. No. 1.4e-17;
Matches 60; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 116 QWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYY 175
Db |||||
1 QWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYY 60

QY 176 ESKA 179
Db |||||
61 ESKA 64

RESULT 34
Q95ZD8
ID Q95ZD8 PRELIMINARY; PRT; 60 AA.
AC Q95ZD8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog protein (Fragment).
GN HEDGEHOG.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaloulis K., Galliot B.;
RT "Hedgehog in Hydra."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011384; CAC50883.1; -;
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH signal; 1.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.

FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 5809 MW; 6624F85A015999CC CRC64;

Query Match 12.1%; Score 298; DB 5; Length 60;
Best Local Similarity 90.0%; Pred. No. 4.5e-15;
Matches 54; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 113 VMNQWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDW 172
Db |||||
1 VMNQWPGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDW 60

RESULT 35
Q90ZR0
ID Q90ZR0 PRELIMINARY; PRT; 56 AA.
AC Q90ZR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Indian hedgehog protein (Fragment).
GN IHH.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Cloning of medaka IHH."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF359590; AAK38706.1; -;
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH signal; 1.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 56
SQ SEQUENCE 56 AA; 6438 MW; 1304032BACD74327 CRC64;

Query Match 11.7%; Score 289; DB 13; Length 56;
Best Local Similarity 94.6%; Pred. No. 1.9e-14;
Matches 53; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 132 GHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHHCYSVKA 187
Db |||||
1 GHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHHCYSVKS 56

RESULT 36
Q866A4
ID Q866A4 PRELIMINARY; PRT; 74 AA.
AC Q866A4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative indian hedgehog protein (Fragment).
GN IHH.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA Petersen J.P., Amling M., Meenen N.M., Haberland M.;
RT "Gene expression patterns in tissue engineered cartilage.";

```
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ536288; CAD60251.1; -
DR InterPro; IPR009045; Hedgehog/DD_pept.
FT NON_TER 1
FT NON_TER 74
SQ SEQUENCE 74 AA; 7839 MW; C5A80F6C2A5F2B45 CRC64;

Query Match 9.9%; Score 245; DB 6; Length 74;
Best Local Similarity 60.8%; Pred. No. 5.3e-11;
Matches 45; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 169 GFDWVYYESKAHHCVSVAENSVAAKSGGCPGSAIVHLEQGGTKLVKDLSPGDRVLAAD 228
Db 1 GFDWVYYESKAHHCVSVAENSVAAKSGGCPGSAIVHLEQGGTKLVKDLSPGDRVLAAMG 60

QY 229 DQGRLLYSDFLTF 242
Db 61 EDGNPTFSVDLIFL 74

RESULT 37
Q9TX33 PRELIMINARY; PRT; 49 AA.
AC Q9TX33;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hedgehog HH protein homolog (Fragment).
DE Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, Genetic linkage and limb patterning activity of a murine
RT hedgehog gene.";
RL Development 120:3339-3353(1994).
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR00320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5607 MW; 0693A628278B72EE CRC64;

Query Match 9.6%; Score 237; DB 5; Length 49;
Best Local Similarity 89.8%; Pred. No. 1.2e-10;
Matches 44; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 119 GVKLRVTEGWDEGDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVE 167
Db 1 GVKLRVTEGWDEGDGHSEESLHYEGRAVDITTSDDRTKYGMLARLAE 49

RESULT 38
Q9TX31 PRELIMINARY; PRT; 49 AA.
AC Q9TX31;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hedgehog HH protein homolog (Fragment).
DE Tribolium castaneum (Red flour beetle).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Polyphaga; Cucujiformia;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
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OC Tenebrionidae; Tribolium.
OX NCBI_TaxID=7070;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, Genetic linkage and limb patterning activity of a murine
RT hedgehog gene.";
RL Development 120:3339-3353(1994).
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR00320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5580 MW; 4A8ECF56DEC99013 CRC64;

Query Match 9.3%; Score 229; DB 5; Length 49;
Best Local Similarity 87.8%; Pred. No. 4.6e-10;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 119 GVKLRVTEGWDEGDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVE 167
Db 1 GVKLRVTEGWDEGDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVE 49

RESULT 39
O42233 PRELIMINARY; PRT; 54 AA.
ID O42233;
AC O42233;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Sonic hedgehog (Fragment).
GN SHH.
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98167903; PubMed=9435297;
RA Borycki A.G., Mendham L., Emerson C.P. Jr.;
RT "Control of somite patterning by Sonic hedgehog and its downstream
RT signal response genes.";
RL Development 125:777-790(1998).
DR EMBL; AF022881; AAB80948.1; -
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR00320; HH_signal.
DR Pfam; PF01085; HH_signal; 1.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 54
FT NON_TER 54
SQ SEQUENCE 54 AA; 5993 MW; D359B0B9DD44E1E9 CRC64;

Query Match 7.6%; Score 188; DB 13; Length 54;
Best Local Similarity 68.6%; Pred. No. 6e-07;
Matches 35; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNV 51
Db 4 MLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYRXPQL 54

RESULT 40
Q9ESH3
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ID Q9ESH3 PRELIMINARY; PRT; 125 AA.
AC Q9ESH3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Indian hedgehog protein (Fragment).
GN IHH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Stevens D.A., Haerterjian R.P., Robson H., van Noorden S., Siebler T.,
RA Shalet S.M., Williams G.R.;
RT "Hypothyroidism causes growth retardation by disrupting chondrocyte
RT differentiation, matrix deposition and endochondral ossification in
RT epiphyseal growth plate cartilage.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF175209; AAC09197.1; -.
DR MEROPS; C46.003; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHOG.
DR SMART; SM00306; HintN; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13648 MW; 8FAEA76826DB45FD CRC64;

Query Match 7.6%; Score 187.5; DB 11; Length 125;
Best Local Similarity 34.9%; Pred. No. 2.1e-06;
Matches 51; Conservative 18; Mismatches 42; Indels 35; Gaps 4;

QY 218 LSPGDRVLAADQGRLLYSDFLTFLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPH 277
Db 7 VKPGDRVLAMGEDGNPTFSVDVLIFLDREPNRLRAFQVIETQDPFRLALTPAHLFIADN 66

QY 278 NDSATGEPEASSGSGPPSGGALGPRALFASRVPRGQRYVYVAERDGRRLLPAAVHSVTL 337
Db 67 H-----AEPAARF-----RATFANHVQPGQYVLV-----AGVQASSL 98

QY 338 -----SEEAAGAYAPLTAQGTILI 356
Db 99 LGWQSPPTWPLGPMLEPSRSMGTLVV 124

RESULT 41
Q9TX32 PRELIMINARY; PRT; 48 AA.
AC Q9TX32;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hedgehog HH protein homolog (Fragment).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, genetic linkage and limb patterning activity of a murine
RT hedgehog gene.";
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RL Development 120:3339-3353(1994).
DR HSSP; Q62226; 1VHH.
DR GO; GO:0007267; P:cell-cell signaling; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR PRINTS; PR00632; SONICHOG.
DR ProDom; PD003042; HH_signal; 1.
FT NON_TER 1
FT NON_TER 48
SQ SEQUENCE 48 AA; 5347 MW; 98A6F87328613DC6 CRC64;

Query Match 7.1%; Score 175.5; DB 5; Length 48;
Best Local Similarity 73.5%; Pred. No. 4.3e-06;
Matches 36; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 119 GVKLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVE 167
Db 1 GIKLRVVEAWDED-QPNVEPLHAEGRAVDITTSDDRKKNKYGALARLAVE 48

RESULT 42
P91573 PRELIMINARY; PRT; 615 AA.
AC P91573;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ZK377.1 protein.
GN ZK377.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierri-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nhan, M., Hawkins J.;
RT "The sequence of C. elegans cosmid ZK377.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88183; AAB52656.1; -.
DR PIR; T29550; T29550.
DR WormPep; ZK377.1; CE15329.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003586; Hedgehog_hintC.
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Db 634 VQEFLLTMT-EYGKTLRITSRHFMYRNKCKGKSPQYIKMLPHD-----GE----- 677

QY 296 GGALGPRALFASRVPGQRVVVAERDGDRLRLPAAVHVSRTLSEEAAGAYAPLTAQGTIL 355

Db 678 -----AIFASDLEVGDCVVVLYKGKRYRQCKIETITRSV-----RTGIYSPLTNNGRII 725

QY 356 INRVLASCYAVIEHS-----WAH 374

Db 726 VNDMLASCYSEIQNTLQTTFFWAY 750

RESULT 45

Q21835

ID Q21835 PRELIMINARY; PRT; 1137 AA.

AC Q21835;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE C. elegans GRD-1 protein (Corresponding sequence R08B4.1a).

GN GRD-1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA White S.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z68008; CAA92000.4; --

KW Homeobox.

SQ SEQUENCE 1137 AA; 123951 MW; 1F061E715F044993 CRC64;

Query Match 5.6%; Score 138.5; DB 5; Length 1137;

Best Local Similarity 24.4%; Pred. No. 0.21;

Matches 50; Conservative 38; Mismatches 68; Indels 49; Gaps 8;

QY 189 NSVAAKSGGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGA 248

Db 923 SALVAATGACFSLDTWV-TTPTGKKRMDQIDIGYVLTADLE-KTYFTPTLWIHREPEK 980

QY 249 KKVFYVIETREPRERLLTAHLLF-----VAPHNDSATGEPEASSGSGPPS 295

Db 981 VQEFLLTMT-EYGKTLRITSRHFMYRNKCKGKSPQYIKMLPHD-----GE----- 1024

QY 296 GGALGPRALFASRVPGQRVVVAERDGDRLRLPAAVHVSRTLSEEAAGAYAPLTAQGTIL 355

Db 1025 -----AIFASDLEVGDCVVVLYKGKRYRQCKIETITRSV-----RTGIYSPLTNNGRII 1072

QY 356 INRVLASCYAVIEHS-----WAH 374

Db 1073 VNDMLASCYSEIQNTLQTTFFWAY 1097

RESULT 46

Q7YXC8

ID Q7YXC8 PRELIMINARY; PRT; 1160 AA.

AC Q7YXC8;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE C. elegans GRD-1 protein (Corresponding sequence R08B4.1b).

GN GRD-1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA White S.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z68008; CAD91696.1; --

KW Homeobox.

SQ SEQUENCE 1160 AA; 125411 MW; 77894C7C7E4A4B11 CRC64;

Query Match 5.6%; Score 138.5; DB 5; Length 1160;

Best Local Similarity 24.4%; Pred. No. 0.22;

Matches 50; Conservative 38; Mismatches 68; Indels 49; Gaps 8;

QY 189 NSVAAKSGGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGA 248

Db 946 SALVAATGACFSLDTWV-TTPTGKKRMDQIDIGYVLTADLE-KTYFTPTLWIHREPEK 1003

QY 249 KKVFYVIETREPRERLLTAHLLF-----VAPHNDSATGEPEASSGSGPPS 295

Db 1004 VQEFLLTMT-EYGKTLRITSRHFMYRNKCKGKSPQYIKMLPHD-----GE----- 1047

QY 296 GGALGPRALFASRVPGQRVVVAERDGDRLRLPAAVHVSRTLSEEAAGAYAPLTAQGTIL 355

Db 1048 -----AIFASDLEVGDCVVVLYKGKRYRQCKIETITRSV-----RTGIYSPLTNNGRII 1095

QY 356 INRVLASCYAVIEHS-----WAH 374

Db 1096 VNDMLASCYSEIQNTLQTTFFWAY 1120

RESULT 47

O45992

ID O45992 PRELIMINARY; PRT; 481 AA.

AC O45992;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE C. elegans WRT-7 protein (Corresponding sequence ZK1037.10).

GN WRT-7.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Basham V.M.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z81142; CAB03509.2; --

SQ SEQUENCE 481 AA; 54512 MW; 4CE81DB2D0AAA962 CRC64;

Query Match 5.4%; Score 134.5; DB 5; Length 481;

Best Local Similarity 24.3%; Pred. No. 0.13;

Matches 45; Conservative 34; Mismatches 67; Indels 39; Gaps 6;

QY 198 CFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLD-----RDDGAKKVF 252
Db 274 CFPNDVAVNVYKAVKRMDELEIGDWVEALDENG-----EDITFLPVKYWLHRDPQEAE 328
QY 253 YVIETREPRERLLTAAHLLFVAPHNDSATCEPEASSGGPPSGGALGPRALFASRVPRG 312
Db 329 FLEFSLDNGETFTLTKHLVY-----JTECRQNS-----SELKISWESISAGKVNAG 375
QY 313 QRVYVVAERDGRRLPAAVHVSRTLSE-----EAAGAYAPLTAQGTILINRVLASCYA 365
Db 376 DCFYLAQSE-----ALTKYRLVEILDIKRVKTKGIYAPMTSQGHLLVNKIHTSCHS 426
QY 366 VIEEH 370
Db 427 EVDHH 431

RESULT 48
Q9XUV2
ID Q9XUV2 PRELIMINARY; PRT; 1021 AA.
AC Q9XUV2;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE K02E2.2 protein.
GN K02E2.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z81560; CAB04547.1; -;
DR PIR; T23252; T23252.
DR HSSP; Q02936; IAT0.
DR WormPep; K02E2.2; CE18837.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016539; P:protein splicing; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR007284; DUF398.
DR InterPro; IPR003586; Hedgehog hintC.
DR InterPro; IPR003587; Hedgehog hint_N.
DR InterPro; IPR006141; Intein S.
DR InterPro; IPR001767; Pept_C46_hint.
DR Pfam; PF04155; DUF398; 4.
DR Pfam; PF01079; Hint; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
SQ SEQUENCE 1021 AA; 115329 MW; E420668EB232D9B7 CRC64;

Query Match 5.1%; Score 126.5; DB 5; Length 1021;
Best Local Similarity 27.1%; Pred. No. 1.4;
Matches 52; Conservative 34; Mismatches 65; Indels 41; Gaps 10;
QY 198 CFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRDDGAKKVFYVIET 257
Db 802 CFSRDTWV-TTPSGKKRMDEIEIGDYVLTADLK-TALFSAITLWIHREPETVQEFLEIKT 859
QY 258 REPRERLLTAAHLLFVA-----PHNDS-----ATGE-----PEASSGGPPSGGAL 299
Db 860 -DNGKTLQLTAGHFYATECRYLPKNSLLNSTPERYRHLIDTLPDDS----- 907

QY 300 GPRALFASRVPRGQRVVVAERDGR-RLLPAAVHVSRTLSEEAAGAYAPLTAQGTILINR 358
Db 908 --ETKLASQLKICECLLI--HNGDQFRMQKIDSISKTVS---TGIYSPLTENGRIYLVND 959
QY 359 VLASCYAVIEEH 370
Db 960 VLASCYSEVQQN 971
RESULT 49
O76786
ID O76786 PRELIMINARY; PRT; 2639 AA.
AC O76786;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fibroin.
OS Antheraea pernyi (Chinese oak silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Saturniidae; Saturniinae; Saturniini; Antheraea.
OX NCBI_TaxID=7119;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496953; PubMed=11040284;
RA Sezutsu H., Yukuhiro K.;
RT "Dynamic rearrangement within the antheraea pernyi silk fibroin gene
is associated with four types of repetitive units."
RL J. Mol. Evol. 51:329-338(2000).
DR EMBL; AF083334; AAC32606.1; -;
DR PIR; T31328; T31328.
SQ SEQUENCE 2639 AA; 216057 MW; 2EE3310DEEB09B9A CRC64;
Query Match 5.0%; Score 123.5; DB 5; Length 2639;
Best Local Similarity 28.5%; Pred. No. 9.2;
Matches 55; Conservative 10; Mismatches 101; Indels 27; Gaps 6;
QY 280 SATGEFEASSGSGPPSGGALGPRALFASRVPRGQRVVVAERDGRRLLPAAVHVSRTLSE 339
Db 2167 AAAAAAAGSGAGRGDGGYGSQ---SSAAAAAARRAGHERAAGSAA----- 2216
QY 340 EAAGAYAPLTAQGTILINRVLASCYAVIEHSHWAHRAPFRLAHALLAALAPARTDRGG 399
Db 2217 -AAAAAASGA---GRSGGS-----YGWGDDGGYGSDDSAASGAGG 2265
QY 400 DSGGDRGGGG--GRVALTPGAADAPGAGATAGIHVYSQLLYQIGTWLLDSEALHPLGM 457
Db 2266 SGGYGGYGGYGSDDSAASGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2321
QY 458 AVKSSXSRGAGGG 470
Db 2322 AAAGSGAGGAGGG 2334

RESULT 50
Q863A2
ID Q863A2 PRELIMINARY; PRT; 702 AA.
AC Q863A2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE T-box 2 transcription factor.
GN TBX2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Andelfinger G., Etter L., Dymont M., Hitte C., Galibert F.,
RA Kirkness E., Benson D.W.;
RT "Exclusion of canine Tbx2 and Tbx4 as candidates for tricuspid valve

RT malformation.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY192802; AAC24699.1; -
DR EMBL; AY192798; AAC24699.1; JOINED.
DR EMBL; AY192799; AAC24699.1; JOINED.
DR EMBL; AY192800; AAC24699.1; JOINED.
DR EMBL; AY192801; AAC24699.1; JOINED.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53-like.
DR InterPro; IPR001699; TF_T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS50252; TBOX_3; 1.
SQ SEQUENCE 702 AA; 73901 MW; 66ADE7D5531D95A3 CRC64;

Query Match 4.9%; Score 122; DB 6; Length 702;
Best Local Similarity 21.2%; Pred. No. 1.8;
Matches 104; Conservative 36; Mismatches 119; Indels 232; Gaps 22;

QY 118 PGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDR-----DRSKYGMRLAR 163
Db | | | | | : | | | | | : | | | | : | | : | |
95 PKVTLEAKELWDQ-----FKLGTGTEWVITKSGRRMFPFVKRVSGLDKKAKYILL-- 144

QY 164 LAVEAGFDWVYYESKAHHCVSVAENS---VAAKSGGCFPGSATVHLEQGGT----- 212
Db : : | | | | | : | | | | : : : : : : : : : :
145 MDIVAADD-----CRYKFHNSRWMVACKADPEMPKRMVYIHEDSPATGEQWMAKP 193

QY 213 -----KLVKDLS-----PGDRVLAADDQGRLLYSDFLTLF----- 242
Db | | | | | : | | | | : : | | | | : : : : : : : : : :
194 VAFHKLKLTNNISDKHGFTILNSMHKYQPRFHIVRANILKLPYSTFTYVFPETDFIAV 253

QY 243 -----DRDDGAKKVYVYVETREPRERLLLTAHLL--FVAPHND 279
Db | | | | : | | | : | | | | : | | | : | | : | | : | |
254 TAYQNDKITQLKIDNPFAGFRDTGNR-----REKRKQLTLPRLYEEHCKPERD 306

QY 280 SATG-----EPEASSGSGPP-----SGGALG 300
Db | | | | | : | | | | : : | | | : | | : | | : | |
307 GAESDASSCDPAPAREPPASPGSAPSLRLHRTADEKCAADSDPEPERLSEERAGPALG 365

QY 301 -----PRALFASRV---RPGQRVVVAERDGD-----RR----- 326
Db | | | | | : | | | | : | | | : | | | : | | : | | : | |
367 RSPGLDGGSPRLTEPERARERRSPERGKEPAESGGDGPFGRLRSLEKERAERKDDGRK 426

QY 327 -----LLPAAVHSVTLSEEAAG-----AYAPLTAQGTILINRVLAS 362
Db | | | | : | | | : | | | : | | | : | | : | | : | |
427 EAGEGKEPGLAPLVVQTDASPLGAGHLPLGAFSGHLHGQQFFGPLGAGQPLFLHP---- 482

QY 363 CYAVIEEHSWAHRAFAFPRFLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGAA- 421
Db : : | | | : | | | : | | | : | | | : | | : | | : | |
483 -----GQFAMGPGAFSAMGMGH-LLASVA-----GGGGGGGGGG-----PGTAT 520

QY 422 --DAPGAGATA 430
Db | | | | : | | : | | : | | : | | : | | : | | : | |
521 GLDAGGLGPAA 531

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 29, 2004, 18:16:03 ; Search time 59 Seconds
(without alignments)
2274.747 Million cell updates/sec

Title: US-09-883-848A-15
Perfect score: 2469
Sequence: 1 MLLIARCLLLVLVSSLLVCS.....GMAVKSSXSRGAGGGAREGA 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2467 | 99.9 | 475 | 2 | AAR77341 Human son |
| 2 | 2467 | 99.9 | 475 | 2 | AAW94473 Human Shh |
| 3 | 2467 | 99.9 | 475 | 2 | AAY05859 Human Son |
| 4 | 2467 | 99.9 | 475 | 2 | AAW97770 Human Son |
| 5 | 2467 | 99.9 | 475 | 2 | AAW05515 Human Son |
| 6 | 2467 | 99.9 | 475 | 3 | AAY96248 Partial h |
| 7 | 2467 | 99.9 | 475 | 3 | AAY70681 Human Son |
| 8 | 2467 | 99.9 | 475 | 3 | AAY95286 Human Son |
| 9 | 2467 | 99.9 | 475 | 3 | AAW95977 Human Son |
| 10 | 2467 | 99.9 | 475 | 4 | AAB84674 Amino aci |
| 11 | 2467 | 99.9 | 475 | 4 | AAB60265 Human Son |
| 12 | 2467 | 99.9 | 475 | 4 | AAE04687 Human son |
| 13 | 2467 | 99.9 | 475 | 4 | AAE05377 Human Son |
| 14 | 2467 | 99.9 | 475 | 4 | AAG65748 Human son |
| 15 | 2467 | 99.9 | 475 | 4 | AAB31222 Amino aci |
| 16 | 2467 | 99.9 | 475 | 5 | ABB79137 Human son |
| 17 | 2467 | 99.9 | 475 | 5 | AAE14297 Human Son |
| 18 | 2467 | 99.9 | 475 | 5 | AAO20923 Human Shh |
| 19 | 2467 | 99.9 | 475 | 5 | AAU99483 Human son |
| 20 | 2467 | 99.9 | 475 | 6 | ADA26256 Human Son |
| 21 | 2467 | 99.9 | 475 | 7 | ADD25260 Human Son |
| 22 | 2467 | 99.9 | 475 | 7 | ABW00868 Human son |
| 23 | 2467 | 99.9 | 475 | 7 | ADD71383 Human son |
| 24 | 2407 | 97.5 | 462 | 4 | AAB85085 Human son |
| 25 | 2407 | 97.5 | 462 | 6 | ADA09286 Human Son |

| | | | | | | | |
|-----|------|------|-----|---|-----------|----------|-----------|
| 99 | 1467 | 59.4 | 418 | 2 | AAW94472 | Aaw94472 | Zebrafish |
| 100 | 1467 | 59.4 | 418 | 2 | AAW94472 | Aay05858 | Zebrafish |
| 101 | 1467 | 59.4 | 418 | 2 | AAW97769 | Aaw97769 | Zebrafish |
| 102 | 1467 | 59.4 | 418 | 2 | AAW95514 | Aay05514 | Zebrafish |
| 103 | 1467 | 59.4 | 418 | 3 | AAW96247 | Aay96247 | Partial z |
| 104 | 1467 | 59.4 | 418 | 3 | AAW96247 | Aay70680 | Zebrafish |
| 105 | 1467 | 59.4 | 418 | 3 | AAW95285 | Aay95285 | Zebrafish |
| 106 | 1467 | 59.4 | 418 | 3 | AAW95976 | Aay95976 | Zebrafish |
| 107 | 1467 | 59.4 | 418 | 4 | AAW95976 | Aab84673 | Amino aci |
| 108 | 1467 | 59.4 | 418 | 4 | AAW95976 | Aab60264 | Zebrafish |
| 109 | 1467 | 59.4 | 418 | 4 | AAW95976 | Aae04686 | Zebrafish |
| 110 | 1467 | 59.4 | 418 | 4 | AAW95376 | Aae05376 | Zebrafish |
| 111 | 1467 | 59.4 | 418 | 4 | AAW95376 | Aab85737 | Zebrafish |
| 112 | 1467 | 59.4 | 418 | 4 | AAW95376 | Aag65747 | Zebrafish |
| 113 | 1467 | 59.4 | 418 | 4 | AAW95376 | Aab31221 | Amino aci |
| 114 | 1467 | 59.4 | 418 | 5 | AAW95376 | Abb79136 | Zebrafish |
| 115 | 1467 | 59.4 | 418 | 5 | AAW95376 | Aae14296 | Zebrafish |
| 116 | 1467 | 59.4 | 418 | 5 | AAW95376 | Aac20922 | Zebrafish |
| 117 | 1467 | 59.4 | 418 | 5 | AAW95376 | Aau99482 | Zebrafish |
| 118 | 1467 | 59.4 | 418 | 6 | AAW95376 | Ada26255 | Zebrafish |
| 119 | 1467 | 59.4 | 418 | 7 | AAW95376 | Add25259 | Zebrafish |
| 120 | 1467 | 59.4 | 418 | 7 | AAW95376 | Abw00867 | Zebrafish |
| 121 | 1467 | 59.4 | 418 | 7 | AAW95376 | Add71382 | Zebrafish |
| 122 | 1432 | 58.0 | 416 | 2 | AAW97658 | Aar97658 | Zebrafish |
| 123 | 1432 | 58.0 | 416 | 2 | AAW97658 | Aaw61485 | Zebrafish |
| 124 | 1432 | 58.0 | 416 | 2 | AAW97658 | Aaw94475 | Zebrafish |
| 125 | 1432 | 58.0 | 416 | 2 | AAW97658 | Aay05862 | Zebrafish |
| 126 | 1432 | 58.0 | 416 | 2 | AAW97771 | Aaw97771 | Zebrafish |
| 127 | 1432 | 58.0 | 416 | 2 | AAW95518 | Aay05518 | Zebrafish |
| 128 | 1432 | 58.0 | 416 | 3 | AAW96251 | Aay96251 | Zebrafish |
| 129 | 1432 | 58.0 | 416 | 3 | AAW970684 | Aay70684 | Zebrafish |
| 130 | 1432 | 58.0 | 416 | 3 | AAW95289 | Aay95289 | Zebrafish |
| 131 | 1432 | 58.0 | 416 | 3 | AAW95980 | Aay95980 | Zebrafish |
| 132 | 1432 | 58.0 | 416 | 4 | AAW95980 | Aab84677 | Amino aci |
| 133 | 1432 | 58.0 | 416 | 4 | AAW95980 | Aab60268 | Zebrafish |
| 134 | 1432 | 58.0 | 416 | 4 | AAW95980 | Aae04706 | Zebrafish |
| 135 | 1432 | 58.0 | 416 | 4 | AAW95980 | Aag65751 | Zebrafish |
| 136 | 1432 | 58.0 | 416 | 5 | AAW95980 | Aae14300 | Zebrafish |
| 137 | 1432 | 58.0 | 416 | 5 | AAW95980 | Aao20926 | Zebrafish |
| 138 | 1432 | 58.0 | 416 | 5 | AAW95980 | Aau99486 | Zebrafish |
| 139 | 1271 | 51.5 | 411 | 2 | AAW94474 | Aaw94474 | Human Ihh |
| 140 | 1271 | 51.5 | 411 | 2 | AAW95860 | Aay05860 | Human Ind |
| 141 | 1271 | 51.5 | 411 | 2 | AAW97763 | Aaw97763 | Human Ind |
| 142 | 1271 | 51.5 | 411 | 2 | AAW95516 | Aay05516 | Human Ind |
| 143 | 1271 | 51.5 | 411 | 3 | AAW96249 | Aay96249 | Human Ihh |
| 144 | 1271 | 51.5 | 411 | 3 | AAW96249 | Aay70682 | Human Ind |
| 145 | 1271 | 51.5 | 411 | 3 | AAW95287 | Aay95287 | Human Ind |
| 146 | 1271 | 51.5 | 411 | 3 | AAW95978 | Aay95978 | Human Ind |
| 147 | 1271 | 51.5 | 411 | 4 | AAW94675 | Aab84675 | Amino aci |
| 148 | 1271 | 51.5 | 411 | 4 | AAW94675 | Aab60266 | Human Ind |
| 149 | 1271 | 51.5 | 411 | 4 | AAW94675 | Aae04688 | Human Ind |
| 150 | 1271 | 51.5 | 411 | 4 | AAW94675 | Aag65749 | Human ind |

ALIGNMENTS

| | |
|-----------|---|
| RESULT 1 | |
| AAW977341 | |
| ID | AAW977341 standard; protein; 475 AA. |
| XX | |
| AC | AAW977341; |
| XX | |
| DT | 14-MAR-1996 (first entry) |
| XX | |
| DE | Human sonic hedgehog protein. |
| XX | |
| KW | Human; sonic hedgehog protein; probe; primer; diagnostic; |
| KW | nervous system disorder; gene therapy; antibody. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| | Location/Qualifiers |

| | | | |
|----|---|---|--|
| FT | Peptide | 24..29 | /note= "conserved sequence (AAR77349)" |
| FT | Misc-difference | 463 | |
| FT | Misc-difference | /note= "unspecified amino acid" | |
| XX | WO9518856-A1. | | |
| XX | 13-JUL-1995. | | |
| PD | 30-DEC-1994; | 94WO-US014992. | |
| PF | 30-DEC-1993; | 93US-00176427. | |
| XX | 14-DEC-1994; | 94US-00356060. | |
| PR | (HARD) HARVARD COLLEGE. | | |
| XX | (IMCR) IMPERIAL CANCER RES TECHNOLOGY. | | |
| PI | Ingham PW, McMahon AP, Tabin CJ; | | |
| XX | WPI; 1995-255060/33. | | |
| DR | N-PSDB; AAQ91639. | | |
| XX | Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful to treat degenerative nervous system disorder(s) and in gene therapy. | | |
| PT | Claim 17; Page 143-45; 210pp; English. | | |
| PT | The sequence represents a human sonic hedgehog protein, homologous to a Drosophila hedgehog protein (AAR77337), and is encoded by a cDNA isolated from a human fetal lung cDNA library. Probes and primers derived from the sonic hedgehog gene may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents | | |
| PS | Sequence 475 AA; | | |
| XX | Query Match | 99.9%; Score 2467; DB 2; Length 475; | |
| XX | Best Local Similarity | 100.0%; Pred. No. 2.1e-217; | |
| XX | Matches | 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 | MLLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60 | |
| Db | 1 | MLLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60 | |
| QY | 61 | RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCXKLNALAI SVMNQWPGV 120 | |
| Db | 61 | RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCXKLNALAI SVMNQWPGV 120 | |
| QY | 121 | KLRVTEGDEDEHHSESLHYEGRAVDITTSDDRSKYGMALARLAVEAGFDWVYESKAH 180 | |
| Db | 121 | KLRVTEGDEDEHHSESLHYEGRAVDITTSDDRSKYGMALARLAVEAGFDWVYESKAH 180 | |
| QY | 181 | IHCSVKAENSVAAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240 | |
| Db | 181 | IHCSVKAENSVAAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240 | |
| QY | 241 | FLDRDDGAKKVPYVIETREPRERLLTLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300 | |
| Db | 241 | FLDRDDGAKKVPYVIETREPRERLLTLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300 | |
| QY | 301 | PRALFASRVPCQRYVVAERDGRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360 | |
| Db | 301 | PRALFASRVPCQRYVVAERDGRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360 | |
| QY | 361 | ASCYAVIEEHSWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420 | |
| Db | 361 | ASCYAVIEEHSWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420 | |
| QY | 421 | ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475 | |
| Db | 421 | ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475 | |

RESULT 2
AAW94473
ID AAW94473 standard; protein; 475 AA.
XX
AC AAW94473;
XX
DT 29-APR-1999 (first entry)
XX
DE Human Shh hedgehog protein sequence.
XX
KW Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;
KW brain infarction; cerebral infarction; transient ischaemic attack;
KW stroke; cerebral infarct volume; spinal cord; oedema; trauma;
KW haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 463
FT /label= unknown
FT /note= "encoded by NNN"
XX
WO9900117-A2.
07-JAN-1999.
26-JUN-1998; 98WO-US013387.
27-JUN-1997; 97US-00883656.
(ONTO-) ONTOGENY INC.
Mahanthappa NK;
WPI; 1999-095458/08.
N-PSDB; AAX16187.
Method for limiting damage to neurons caused by ischaemic or epoxic conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks.
Disclosure; Page 72-74; 104pp; English.
A method has been developed for limiting the damage to neuronal cells by ischaemic or epoxic conditions by administering a ptc (patched) therapeutic agent to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombotic or embolic) and transient ischaemic attacks. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,%. The present sequence represents a hedgehog sequence given in the present invention
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MLLARCLLLVLSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 1 MLLARCLLLVLSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYNPDIIIPKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYNPDIIIPKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRDRSKYKMLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRDRSKYKMLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQVRVYVVAERDGDRLLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQVRVYVVAERDGDRLLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPAPFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPAPFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSXSRGAGCGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSXSRGAGCGGAREGA 475

RESULT 3
AAV05859
ID AAV05859 standard; protein; 475 AA.
XX
AC AAV05859;
XX
DT 02-AUG-1999 (first entry)
XX
DE Human Sonic hedgehog Shh protein.
XX
KW Sonic hedgehog; Shh; human; epithelial tissue; epithelium;
KW cutaneous tissue; skin; hair; wound healing; vulneryary; burn;
KW skin grafting; pressure sore; ulcer; ulcerative colitis; alopecia;
KW psoriasis; keratosis; acne; comedogenic lesion; folliculitis;
KW pseudo-folliculitis; keratoacanthoma; callosities; Darier's disease; scar;
KW autoimmune disease; pemphigus; epidermolysis; lupus lesion;
KW desquamative lesion; carcinoma; therapy; hedgehog therapeutic;
KW ptc therapeutic; patched.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 463
FT /note= "encoded by NNN"
XX
PN WO9920298-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US022227.
XX
PR 20-OCT-1997; 97US-00955552.
PR 11-SEP-1998; 98US-00151999.
XX
PA (ONTO-) ONTOGENY INC.
XX
PI Wang EA;
XX
DR WPI; 1999-288170/24.
DR N-PSDB; AAX25622.
XX
PT Use of hedgehog polypeptides on patched therapeutics.
XX
PS Claim 26; Page 127-128; 146pp; English.

XX The present sequence represents human Sonic hedgehog protein Shh. The
CC invention relates to a method for modulating the growth state an
CC epithelial cell by ecotopically contacting the epithelial cell, in vitro
CC or in vivo, with a hedgehog therapeutic (i.e. a hedgehog polypeptide or
CC gene therapy construct) or ptc therapeutic (i.e. a small organic molecule
CC that mimics the effect of hedgehog proteins on patched signalling, or
CC activates or potentiates patched signalling) in an amount effective to
CC alter the rate of proliferation of the epithelial cell. The hedgehog
CC therapeutic preferably comprises at least a bioactive extracellular
CC portion of a hedgehog protein (see AAY05854-62) encoded by a vertebrate
CC hedgehog gene (see AAX25617-25), especially a human hedgehog gene.
CC Promotion of proliferation of epithelial cells can be used to control a
CC wound healing process in e.g. burn treatment, skin regeneration, skin
CC grafting, pressure sore treatment, dermal ulcer treatment, post surgery
CC scar reduction or treatment of ulcerative colitis (claimed). It can also
CC be used to induce hair growth for the treatment of alopecia (claimed).
CC Inhibition of the growth of epithelial tissue can be used to treat or
CC prevent hyperplastic or neoplastic conditions, e.g. psoriasis, keratosis,
CC acne, comedogenic lesions, folliculitis and pseudofolliculitis,
CC keratoacanthoma, callosities, Darier's disease, keloids, hypertrophic
CC scars, or autoimmune disorders, e.g. aphthous ulcers, pemphigus vulgaris,
CC pemphigus foliaceus, pemphigus vegetans, pemphigus erythematous,
CC epidermolysis, lupus lesions, desquamative lesions or carcinomas. The
CC methods can also be used to counteract the effects of ageing on skin
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSSLLVCSGLACGGRGFGKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
DB 1 MLLARCLLLVSSLLVCSGLACGGRGFGKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
DB 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
DB 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
DB 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVPYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
DB 241 FLDRDDGAKKVPYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGORVYVVAERDGRRLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
DB 301 PRALFASRVPRGORVYVVAERDGRRLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAPFAPFRLAHALLAALAPARTDRGDSGGGDRGGGRVALTAPGA 420
DB 361 ASCYAVIEHSHWAHRAPFAPFRLAHALLAALAPARTDRGDSGGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAKSSXSRGAGGGGAREGA 475
DB 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAKSSXSRGAGGGGAREGA 475

RESULT 4
AAW97770
ID AAW97770 standard; protein; 475 AA.
XX
AC AAW97770;
XX
DT 21-MAY-1999 (first entry)
XX

DE Human Sonic hedgehog (Shh) protein.
XX
KW Sonic hedgehog; Shh protein; human; dopaminergic; GABA-nergic;
KW ptc therapeutic; patched; signal transduction; Parkinson's disease;
KW Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia;
KW hypoxia; neuroprotective; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 463 /note= "encoded by NNN"
XX
FN WO9904775-A2.
XX
PD 04-FEB-1999.
XX
PF 24-JUL-1998; 98WO-US015419.
XX
PR 24-JUL-1997; 97US-00900220.
XX (ONTO-) ONTOGENY INC.
PA Miao N, Wang M, Mahanthappa NK, Pang K;
PI WPI; 1999-142578/12.
XX N-PSDB; AAX07276.
DR
DR Increasing the survival of neuronal, dopaminergic and GABA-nergic cells -
PT by using a ptc therapeutic such as a protein kinase inhibitor, or an
PT agent derived from hedgehog polypeptides, useful in the treatment of
PT Parkinson's disease.
XX
XX Disclosure; Page 93-95; 138pp; English.
XX
CC This polypeptide is human Shh Sonic hedgehog protein. The invention is
CC based on the finding that hedgehog proteins are useful as protective
CC agents in the treatment and prophylaxis of neurodegenerative disorders
CC resulting from the loss of dopaminergic and/or GABA-nergic neurons, or
CC the general loss of tissue from the substantia nigra. Exemplary disorders
CC include Parkinson's disease, Huntington's disease (both claimed),
CC amyotrophic lateral sclerosis and cerebral ischaemia. The invention
CC relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene
CC therapy constructs e.g. constructs encoding recombinant hedgehog
CC polypeptides and trans-activation constructs for altering hedgehog gene
CC regulatory sequences) and ptc therapeutics (i.e. agents which mimic the
CC effect of naturally occurring hedgehog proteins on patched signalling)
CC that are effective in both human and animal subjects. Human ihh and Dhh
CC polypeptides (see AAW97763-64) are preferred. The products can also be
CC used for the maintenance of differentiated neurons in cultures, and to
CC enhance the implantation of such neuronal cells in an animal. They can be
CC used to prevent or treat neurodegenerative conditions arising from the
CC use of certain drugs, and in the prevention and/or treatment of hypoxia,
CC e.g. as a neuroprotective agent
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSSLLVCSGLACGGRGFGKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
DB 1 MLLARCLLLVSSLLVCSGLACGGRGFGKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
DB 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
DB 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSVAAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQVVVAERDGDRLRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVAERDGDRLRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 5
AA05515
ID AAY05515 standard; protein; 475 AA.
XX
AC AAY05515;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Sonic hedgehog protein Shh.
XX
KW Sonic hedgehog; Shh protein; human; hedgehog therapeutic;
KW ptc therapeutic; patched; signal transduction; muscle atrophy; cachexia;
KW muscular myopathy; myoblastic sarcoma; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 463
FT /note= "encoded by NNN"
XX
PN WO9910004-A2.
XX
PD 04-MAR-1999.
XX
PF 28-AUG-1998; 98WO-US017922.
XX
PR 29-AUG-1997; 97US-0057394P.
XX
PA (ONTO-) ONTOGENY INC.
XX
PI Bladgen CS, Currie PD, Ingham PW, Hughes SM;
XX
XX WPI; 1999-243557/20.
DR N-PSDB; AAX25103.
XX
PT A new method to regulate muscle growth.
XX
PS Disclosure; Page 118-120; 130pp; English.
XX

CC The present sequence is human Sonic hedgehog protein Shh. The invention
CC relates to a method for modulating the formation and/or maintenance of
CC muscle tissue by ecotopically contacting muscle cells, especially muscle
CC stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic
CC (i.e. hedgehog polypeptides and gene therapy constructs) or ptc
CC therapeutic (i.e. a small organic molecule that mimics the effect of
CC hedgehog proteins on patched signalling, or activates or potentiates
CC patched signalling) in an amount effective to alter the growth state of
CC the treated cells. Also claimed is a method for treatment or prevention
CC of disorders of, or surgical or cosmetic repair of, such muscle tissues,
CC by administering a hedgehog polypeptide or ptc therapeutic. The disorder
CC may be muscle atrophy, in particular skeletal muscle atrophy or cardiac
CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The

CC hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic-
CC derived tissue to provide treatment of hyperblastic or neoplastic growth
CC of muscle tissue such as in myoblastic sarcoma (also claimed). The
CC hedgehog therapeutic preferably comprises at least a bioactive
CC extracellular portion of a hedgehog protein (see AAY05510-19) encoded by
CC a vertebrate hedgehog gene (see AAX25098-107), especially a human
CC hedgehog gene
XX
SQ Sequence 475 AA;
Query Match 99.9%; Score 2467; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRHPKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNPNPDIIIFKDEENTGADRMTQRCCKLNALAISVNMQWPGV 120
Db 61 RYEGKISRNSERFKELTPNPNPDIIIFKDEENTGADRMTQRCCKLNALAISVNMQWPGV 120
QY 121 KLRVTEGWDEGHHSEESLHYEGRAVDITTSDDRKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEGHHSEESLHYEGRAVDITTSDDRKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQVVVAERDGDRLRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVAERDGDRLRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 6
AA05515
ID AAY96248 standard; protein; 475 AA.
XX
AC AAY96248;
XX
DT 11-SEP-2000 (first entry)
XX
DE Partial human Shh.
XX
KW Human; sonic hedgehog; Shh; neuromuscular disorder; neuropathy;
KW Guillain-Barre syndrome; peripheral neuropathy; diabetes; alcoholism;
KW chronic inflammatory demyelinating polyneuropathy; CIPD; gene therapy;
KW infection; inflammation; hereditary neuropathy;
KW Charcot-Marie-Tooth disease; vasculitis; lung cancer; tumour;
KW multiple myeloma; nutritional imbalance; kidney disease;
KW hypothyroid neuropathy; trauma; Refsum's disease; Abetalipoproteinemia;
KW Tangier disease; Krabbe's disease; Metachromatic leukodystrophy;
KW Fabry's disease; CMT; GBS; Dejerine-Sottas syndrome; acute neuropathy;
KW Amyotrophic lateral sclerosis; ALS; Miller-Fisher syndrome; amyloidosis;
KW Hereditary sensory neuropathy Type II; HSN II; B-cell lymphoma;
KW Waldenstrom's Macroglobulinaemia; Chronic lymphocytic leukaemia;
KW neuroprotective; cytoprotective; patched-mediated signal transduction.
XX
OS Homo sapiens.
XX

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FH Key Location/Qualifiers
FT Misc-difference 463
FT /label= unknown
FT /note= "Encoded by NNN"
XX WO200027422-A2.
XX
PD 18-MAY-2000.
XX
PF 08-NOV-1999; 99WO-US026334.
XX
PR 06-NOV-1998; 98US-00187387.
XX
PA (BIOJ ) BIOGEN INC.
PA (ONTO-) ONTOGENY INC.
XX
PI Galdes A, Mahanthappa N;
XX
DR WPI; 2000-387341/33.
DR N-PSDB; AAA30279.
XX
PT Novel method of preventing deterioration of peripheral nerves, useful for
PT treating or preventing neuropathy, e.g. where associated with diabetes or
PT viral infection, by administering hedgehog or patched agent.
XX
PS Claim 7; Page 134-135; 152pp; English.
XX
CC The present sequence is the partial human sonic hedgehog protein, Shh.
CC This sequence inhibits expression of the patched gene which has been
CC implicated in neuromuscular disorders (neuropathies). This sequence may
CC therefore be used for treating neuromuscular disorders i.e. preventing
CC degradation in function of motor or sensory nerves and protecting
CC peripheral nerve cells under conditions that normally cause neuropathy. A
CC variety of neuromuscular disorders may be treated: Guillain-Barre
CC syndrome, GBS; peripheral neuropathy; diabetic neuropathy; alcohol-
CC induced neuropathy; chronic inflammatory demyelinating polyneuropathy,
CC CIPD; infection-induced neuropathy, including HIV infection; inflammation
CC -induced neuropathy; hereditary neuropathy e.g. Charcot-Marie-Tooth
CC disease (CMT), Familial Amyloidotic neuropathy, Refsum's disease,
CC Abetalipoproteinemia, Tangier disease, Dejerine-Sottas syndrome, Hereditary
CC leukodystrophy, Fabry's disease, Dejerine-Sottas syndrome, Hereditary
CC sensory neuropathy Type II (HSN II) and Amyotrophic lateral sclerosis
CC (ALS); acute neuropathy e.g Miller-Fisher syndrome; neuropathy caused by
CC vasculitis; neuropathy associated with tumours e.g. lung cancer, multiple
CC myeloma, B-cell lymphoma, Waldenstrom's Macroglobulaemia, Chronic
CC Lymphocytic Leukaemia; neuropathy associated with: amyloidosis,
CC nutritional imbalance, kidney disease, trauma; and hypothyroid
CC neuropathy. The coding sequence may be used in gene therapy of the above
CC disorders
XX
SQ Sequence 475 AA;
Query Match 99.9%; Score 2467; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVYSSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
Db 1 MLLARCLLLVYSSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITSDRRSKYGMRLARLAVEAGFDWVYVESKAH 180
Db 121 KLRVTEGWDEGHSEESLHYEGRAVDITSDRRSKYGMRLARLAVEAGFDWVYVESKAH 180
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
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Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVRPQQRVYVVAERDGERLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVRPQQRVYVVAERDGERLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFPRLAHALLAALAPARTDRGGSGGDRGGGGRVALTPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFPRLAHALLAALAPARTDRGGSGGDRGGGGRVALTPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475
RESULT 7
AAAY70681
ID AAAY70681 standard; protein; 475 AA.
XX
AC AAAY70681;
DT 18-JUL-2000 (first entry)
XX
DE Human Sonic hedgehog (Shh) protein.
XX
KW Sonic hedgehog; Shh; human; growth modulator; therapeutic agent; lung;
KW hedgehog; hh; patched; ptc; fibroblast growth factor; fgf-10;
KW antiproliferative; anticancer; vulnery; antirheumatic; hypotensive;
KW anti-inflammatory; antiasthmatic; antiarthritic; tuberculostatic; asthma;
KW antimicrobial; antiallergy; treatment; prevention; lung diseases; cancer;
KW cystic fibrosis; bronchitis; emphysema; respiratory distress syndrome;
KW tuberculosis; wound healing; lung transplantation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 463
FT /label= Unknown
FT /note= "Encoded by NNN"
XX
WO2000015246-A2.
XX
PD 23-MAR-2000.
XX
PF 10-SEP-1999; 99WO-US020500.
XX
PR 11-SEP-1998; 98US-0099952P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Pepicelli C, Lewis P, McMahon AP;
XX
DR WPI; 2000-271252/23.
DR N-PSDB; AAZ52262.
XX
PT Modulation of lung tissue or cell growth rate used for treating or
PT preventing damage to lung tissue comprises ectopically contacting tissue
PT with hedgehog therapeutic, patched therapeutic or fibroblast growth
PT factor-10.
XX
PS Claim 14; Page 124-127; 143pp; English.
XX
CC The patent discloses a method for modulating the growth state of
CC epithelial or mesenchymal cells of the lung, by ectopically contacting
CC the tissue with a therapeutic agent, that can effectively alter the rate
CC of proliferation of cells. This agent can be selected from hedgehog (hh),
CC patched (ptc) or fibroblast growth factor (fgf)-10 therapeutics. It
CC involves a direct or indirect antagonism of patched-mediated regulation
CC of gene expression. This method is useful for the treatment or prevention
CC of lung diseases, like cancer, cystic fibrosis, bronchopneumoconiosis,
CC bronchitis, bronchospasm, sarcoidosis, silicosis, eosinophilic granuloma,
CC ankylosing spondylitis, emphysema, tuberculosis, respiratory distress
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CC syndrome, allergic rhinitis, asthma, pulmonary fibrosis and primary
CC pulmonary hypertension. It is also used to control wound healing or other
CC reformation processes in the lung and augment lung transplantation. The
CC present sequence is the human sonic hedgehog (Shh) protein, essential for
CC development of the respiratory system. Hedgehog polypeptides can be used
CC to control the formation and/or maintenance of the lung tissue
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLLTPLAYKQFIPNVAEKTILGASG 60
Db |||||
1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db |||||
61 RYEGKISRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db |||||
121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db |||||
181 IHCSVKAENSVAAKSGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
Db |||||
241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQRYVYVAERDGDRLLPAAVHVSVTLSAEAGAYAPLTAQGTILINRVL 360
Db |||||
301 PRALFASRVPRGQRYVYVAERDGDRLLPAAVHVSVTLSAEAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db |||||
361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db |||||
421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 8
AA95286
ID AA95286 standard; protein; 475 AA.

AC AA95286;

DT 12-SEP-2000 (first entry)

XX Human Sonic hedgehog Shh protein.

XX Sonic hedgehog; Shh; human; excitotoxicity; Parkinson's disease;
KW Huntington's disease; neuronal degeneration; neuroprotective;
KW dopaminergic; GABAergic; substantia nigra; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 463 /note= "encoded by NNN"

PN WO200035948-A1.

XX 22-JUN-2000.

XX 03-DEC-1999; 99WO-US028721.

XX 03-DEC-1998; 98WO-US025676.

PR 27-JAN-1999; 99US-00238243.
PR 03-JUN-1999; 99US-00325602.
XX (BIOJ) BIOGEN INC.
PA (ONTO-) ONTOGENY INC.
XX Galdes A, Mahanthappa N;
XX WPI; 2000-431570/37.
DR N-PSDB; AAA27881.

PT Treating disorders involving exotoxicity, e.g. trauma, hypoglycemia,
PT senile dementia and Korsakoff's disease, by using lipophilic modified
PT hedgehog polypeptide.

PS Disclosure; Page 157-159; 174pp; English.

XX The present sequence of that of human Sonic hedgehog (Shh) protein. The
CC invention relates to a method for promoting the survival and/or
CC functional performance of neuronal cells, especially substantia nigra,
CC dopaminergic or GABAergic neurons that are susceptible to exotoxicity, by
CC contacting the cells, in vitro or in vivo, with a lipophilic (e.g.
CC cholesterol) modified hedgehog polypeptide. The method is used to treat
CC or prevent Parkinson's disease, Huntington's disease, domoic acid
CC poisoning, spinal cord trauma, hypoglycemia, mechanical trauma to the
CC nervous system, senile dementia, Korsakoff's disease, schizophrenia, AIDS
CC dementia, multi-infarct dementia, mood disorders, depression, chemical
CC toxicity, neuronal damage associated with uncontrolled seizures such as
CC epileptic seizures, neuronal injury associated with HIV and AIDS,
CC neurodegeneration associated with Down's syndrome, neuropathic pain
CC syndrome, olivopontocerebral atrophy, amyotrophic lateral sclerosis,
CC mitochondrial abnormalities, Alzheimer's disease, hepatic encephalopathy,
CC Tourette's syndrome and drug addiction (all claimed). The lipophilic
CC modified hedgehog polypeptide is also useful for promoting survival
CC and/or functional performance of neuronal cells susceptible to
CC exotoxicity

XX SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLLTPLAYKQFIPNVAEKTILGASG 60
Db |||||
1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db |||||
61 RYEGKISRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db |||||
121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db |||||
181 IHCSVKAENSVAAKSGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
Db |||||
241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQRYVYVAERDGDRLLPAAVHVSVTLSAEAGAYAPLTAQGTILINRVL 360
Db |||||
301 PRALFASRVPRGQRYVYVAERDGDRLLPAAVHVSVTLSAEAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db |||||
361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db |||||

Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

RESULT 9

AA95977

ID AAY95977 standard; protein; 475 AA.

XX AAY95977;

AC AAY95977;

XX 05-DEC-2000 (first entry)

XX Human Sonic hedgehog Shh protein.

DE Sonic hedgehog; Shh; human; agonist; antagonist; lipid modulator;

XX vacuole; cholesterol disorder; lipid disorder; lipid metabolism;

XX lipid storage; lipid transport; apolipoprotein; triglyceride;

KW hypercholesterolemia; abetalipoproteinemia; hypobetalipoproteinemia;

KW chylomicron retention; Anderson's disease; fat absorption;

KW atherosclerosis; obesity; weight loss; vitamin A disorder;

KW vitamin E disorder; antilipemia; anorectic; antiarteriosclerotic;

XX gene therapy; diagnosis.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FH Misc-difference 463 /note= "encoded by NNN"

FT

XX WO200051628-A2.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US005662.

XX 03-MAR-1999; 99US-0122640P.

PR 15-MAR-1999; 99US-0124446P.

XX

XX (BIOJ) BIOGEN INC.

XX

XX Burkly L, Wang LC;

PI WPI; 2000-611340/58.

XX N-PSDB; AAA95977.

DR

XX

XX Use of lipid modulators (e.g. hedgehog agonists or antagonists) for

PT modulating lipid metabolism and storage, especially useful for treating

PT lipid metabolism or cholesterol disorders, e.g. obesity or

PT hypercholesterolemia.

XX

PS Disclosure; Page 118-120; 136pp; English.

XX

XX The present sequence of that of human Sonic hedgehog (Shh) protein. The

CC invention provides claimed methods for modulating lipid metabolism, for

CC modulating vacuole formation in intestinal epithelial cells, for

CC modulating the accumulation of fat in intestinal epithelial cells, for

CC treating a cholesterol disorder and for treating a lipid metabolism

CC disorder in an animal (especially a human) by administering a lipid

CC modulator selected from a hedgehog antagonist or hedgehog agonst. In

CC particular, the lipid metabolism disorder is a lipid storage disorder, a

CC lipid transport disorder, an apolipoprotein disorder, a triglyceride

CC disorder, e.g. a triglyceride metabolism disorder, a triglyceride

CC transport disorder or a triglyceride storage disorder; a diet-induced

CC hypercholesterolemia, hypercholesterolemia, abetalipoproteinemia,

CC hypobetalipoproteinemia; a chylomicron-retention disorder, Anderson's

CC disease, a fat absorption disorder, e.g. obesity or associated with

CC weight loss, normotriglyceridemic abetalipoproteinemia, an apolipoprotein

CC -B100 deficiency, a fat soluble vitamin disorder, where the fat soluble

CC vitamin is vitamin A or E, or atherosclerosis (all claimed). The hedgehog

CC antagonist binds to the hedgehog receptor, but does not elicit a

CC response. It is preferably a hedgehog mimetic, a modified hedgehog

CC protein, e.g. an inactive hedgehog variant, or an anti-hedgehog

CC homologue, especially a human, chimeric or humanised antibody. The

CC methods are useful in preventing these disorders or protecting a subject

CC from these disorders. The hedgehog antagonist and agonist are also useful

CC in diagnosis and research associated with these disorders. The lipid

CC modulators may also be used as a part of a gene therapy protocol to

CC deliver polynucleotides encoding these lipid modulators

XX

SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 3; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.1e-217;

Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVLSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQIPNVAEKTLCASG 60

DB 1 MLLARCLLLVLSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQIPNVAEKTLCASG 60

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQPGV 120

DB 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQPGV 120

QY 121 KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

DB 121 KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

DB 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFYVIETREPRERLLTLTAHLLFVAPHNDSATGEPEASSGGPPSGGALG 300

DB 241 FLDRDDGAKKVFYVIETREPRERLLTLTAHLLFVAPHNDSATGEPEASSGGPPSGGALG 300

QY 301 PRALFASRVPRGQRVVVAERDGRRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

DB 301 PRALFASRVPRGQRVVVAERDGRRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

DB 361 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

DB 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

RESULT 10

AA84674

ID AAB84674 standard; protein; 475 AA.

XX

AC AAB84674;

XX

DT 17-SEP-2001 (first entry)

XX

DE Amino acid sequence of a human hedgehog (Shh) polypeptide.

XX

KW Shh gene; hedgehog gene; T lymphocyte; patched gene; infection; diabetes;

KW nutritional deficiency; graft rejection; hyperacute response;

KW cornea transplant; autoimmune disorder; multiple sclerosis; psoriasis;

KW atopic dermatitis; inflammatory disease; proliferative disease;

KW hyperproliferative disease; eczematous dermatitis; urticaria; vasculitis;

KW scleroderma.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 463 /note= "unspecified residue encoded by NNN"

XX

PN WO200140438-A2.

XX

PD 07-JUN-2001.

XX

PF 30-NOV-2000; 2000WO-US032590.

XX

PR 30-NOV-1999; 99US-0168112P.
XX (CURI-) CURIS INC.
PA Crompton T;
XX WPI; 2001-441484/47.
DR N-PSDB; AAH28451.
XX
PT Modulating immune function comprises administration of a hedgehog or ptc
PT agent, for treating e.g. diabetes, eczematous dermatitis, urticaria or
XX vasculitis.
PS Claim 4; Page 84-86; 105pp; English.
XX
CC The present sequence represents a hedgehog (Shh) polypeptide. Hedgehog
CC gene products and signal transduction pathways involving hedgehog are
CC involved in the maturation of T lymphocytes. The specification describes
CC a method for modulating immune function, by administration of a hedgehog
CC or patched (ptc) polypeptide, agonists or antagonists. The method is used
CC to treat disorders affecting the regulation of lymphocytes, particularly
CC maturation and/or activation of T lymphocytes. It is used to treat
CC bacterial or viral infection, diabetes, nutritional deficiencies, graft
CC rejection or other hyperacute response such as kidney, heart, lung, bone
CC marrow spleen skin or cornea transplant or autoimmune disorders such as
CC multiple sclerosis, psoriasis or atopic dermatitis. The method is used to
CC treat inflammatory, proliferative and hyperproliferative diseases, as
CC well as cutaneous manifestations of immunological disorders such as
CC eczematous dermatitis, urticaria, vasculitis and scleroderma
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGASG 60
DB 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQPGV 120
DB 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSRDRSKYGLMARLAVEAGFDWVYYESKAH 180
DB 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSRDRSKYGLMARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCPGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
DB 181 IHCSVKAENSVAAKSGGCPGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
DB 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQVVVVAERDGDRLRLPAAVHVSVTLSAEAGAYAPLTAQGTILINRVL 360
DB 301 PRALFASRVPRGQVVVVAERDGDRLRLPAAVHVSVTLSAEAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
DB 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
DB 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 11
AAB60265
ID AAB60265 standard; protein; 475 AA.
XX

AC AAB60265;
XX 30-MAR-2001 (first entry)
DT Human Sonic hedgehog (Shh) protein, SEQ ID NO:15.
XX
DE Hedgehog protein; polymer conjugate; polyalkene glycol group;
XX bioavailability; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour.
XX
OS Homo sapiens.
XX WO200073337-A1.
PN 07-DEC-2000.
PD 26-MAY-2000; 2000WO-US014741.
XX 01-JUN-1999; 99US-0137011P.
PR 13-AUG-1999; 99US-0149016P.
XX (BIOJ) BIOGEN INC.
PA Pepinsky RB, Taylor F, Garber E;
PI WPI; 2001-049927/06.
DR N-PSDB; AAF27018.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's disease
PT and Huntington's chorea, comprises a polymer containing a polyalkylene
PT glycol group linked to any residue other than the N-terminal and lysine
PT residues.
XX
PS Disclosure; Page 138-140; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
CC glycol group, with the proviso that the polymer is not conjugated to the
CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
CC a hedgehog fusion protein. The invention also relates to methods of
CC defining and mapping functionally important regions of a protein by
CC modifying accessible amino acid side chains, and determining the effect
CC the position and/or type of modification have on the activity of the
CC protein. The hedgehog polymer conjugates may be used in the management of
CC various medical conditions including various neurological disorders,
CC inflammatory and autoimmune diseases, and cancers. In particular, they
CC may be used to prevent preventing or ameliorate neurodegenerative
CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
CC disease); age-associated neurological disease; neurological injury and
CC trauma; immunological diseases of the nervous system (e.g., multiple
CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
CC neuroectodermal tumours. The modifications made to the hedgehog protein
CC may result in increased half-life, altered tissue distribution (such as
CC an improved ability to stay in the vasculature for longer periods of
CC time), increased stability in solution, protection from proteolytic
CC degradation, or reduced immunogenicity. In particular, the ability to
CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a member
CC of the hedgehog family of proteins
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Human Sonic hedgehog protein.

KW Human; Sonic hedgehog; Shh; morphogenic signal; neuron; chromosome 7q;

DE embryonic patterning; cell culture; cell differentiation; ischaemia;

XX cell proliferative disorder; intracerebral grafting; Huntington's chorea;

KW neurological disorder; Alzheimer's disease; Parkinson's disease;

KW amyotrophic lateral sclerosis; ALS; multiple sclerosis.

XX Homo sapiens.

OS Key Location/Qualifiers

XX Key Location/Qualifiers

FT Misc-difference 463

FT /label= Unknown

FT /note= "Encoded by NNN"

XX US6261786-B1.

PN 17-JUL-2001.

XX 02-JUL-1996; 96US-00674509.

XX 30-DEC-1993; 93US-00176427.

PR 14-DEC-1994; 94US-00356060.

PR 04-MAY-1995; 95US-00435093.

PR 05-JUN-1995; 95US-00460900.

PR 05-JUN-1995; 95US-00462386.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

PA (HARD) HARVARD COLLEGE.

XX Marigo V, Tabin CJ, Ingham PW, McMahon AP;

PI WPI; 2001-440859/47.

XX N-PSDB; AAD10151.

DR Screening compounds that potentiate or inhibit binding of hedgehog

XX polypeptide to naturally occurring patched receptor, comprises contacting

PT polypeptide with receptor and test compound, and detecting change in

PT binding.

XX Claim 2; Col 163-166; 127pp; English.

XX The present invention relates to assay for screening compounds that

CC potentiate or inhibit binding of hedgehog polypeptide to naturally

CC occurring patched receptor. The hedgehog proteins comprise morphogenic

CC signals produced by embryonic patterning centres, and are involved in the

CC formation and maintenance of ordered spatial arrangements of

CC differentiated tissues in vertebrates, both adult and embryonic. The

CC proteins can be used to generate and/or maintain an array of different

CC vertebrate tissues both in vitro and in vivo. The invention also relates

CC to a method for modulating growth, differentiation or survival of a

CC mammalian cell (e.g. neuron, testicular cell) responsive to hedgehog

CC induction. Hedgehog agonists and antagonists can be used in cell culture

CC techniques to enhance survival and maintenance of neurons and various

CC vertebrate organogenic pathways. The hedgehog gene is useful in

CC determining whether a patient is at the risk of disorder characterised by

CC unwanted cell proliferation or aberrant control of differentiation. The

CC hedgehog proteins or mimetics can be used to induce foetal neurons

CC especially neuronal stem cells in intracerebral grafting. The protein or

CC its mimetic can be used in the treatment of neurological conditions e.g.

CC injury to nervous system, ischaemia resulting from stroke, Alzheimer's

CC disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral

CC sclerosis (ALS) and multiple sclerosis. The present sequence is human

CC Sonic hedgehog (Shh) protein. The Shh gene is located on human chromosome

XX 7q

SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 4; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.1e-217;

Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

Db 1 MLLARCLLLVSSLLVCSGLACGPRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 120

Db 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 120

QY 121 KLRVTEGWDEGHSEESILHYEGRADVITTSRDRSKYGMRLARLAVEAGFDWVYESKAH 180

Db 121 KLRVTEGWDEGHSEESILHYEGRADVITTSRDRSKYGMRLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCPGGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSVKAENSVAAKSGGCPGGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFIETREPRERLLTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300

Db 241 FLDRDDGAKKVFIETREPRERLLTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300

QY 301 PRALFASRVVRPGQRVVVAERDGGRRLLPAAVHVSVTLSAAAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVVRPGQRVVVAERDGGRRLLPAAVHVSVTLSAAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFAPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420

Db 361 ASCYAVIEHSHWAHRAFAFAPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWYSOLLVQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

Db 421 ADAPGAGATAGIHWYSOLLVQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 14

AAG65748

ID AAG65748 standard; protein; 475 AA.

XX AAG65748;

XX 07-JAN-2002 (first entry)

XX Human sonic hedgehog (Shh) polypeptide.

XX Adipocyte; hedgehog polypeptide; desert hedgehog; indian hedgehog; Dhh;

KW Ihh; sonic hedgehog; Shh; therapeutic; cytostatic; tumor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 463

FT /note= "encoded by NNN"

XX WC200164238-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006450.

XX 29-FEB-2000; 2000US-0186058P.

XX (CURI-) CURIS INC.

XX Zehentner B, Leser-Reiff U, Buttscher H;

XX WPI; 2001-607352/69.

DR N-PSDB; AAI66776.

XX Method for regulating formation and/or maintenance of adipocyte tissue by

PT contacting pre-adipocyte or adipocyte cells with a hedgehog polypeptide

PT or ptc therapeutic.

XX Disclosure; Page 102-104; 132pp; English.

PS

XX

CC The invention provides a method for regulating formation and/or
CC maintenance of adipocyte tissue that comprises contacting pre adipocyte
CC or adipocyte cells with a hedgehog polypeptide or ptc therapeutic. The
CC method is used for regulating the growth state of an adipocyte stem/
CC progenitor cell, and treating or preventing disorders of, or surgical or
CC cosmetic repair of, adipocyte tissues, e.g. for treating or preventing
CC hyperplastic or neoplastic conditions affecting adipocyte tissue, such as
CC soft tissue tumors, especially adipose cell tumors, e.g. lipomas,
CC fibrolipomas, lipoblastomas, lipomatosis, hibernomas, hemangiomas and/or
CC liposarcomas. Hedgehog polypeptides can be used in combination with other
CC therapeutic agents. The present sequence represents a human sonic
CC hedgehog (Shh) polypeptide
XX
SQ

Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
DB 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
DB 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
DB 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
DB 181 IHCSVKAENSVAAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
DB 241 FLDRDDGAKKVFYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQRYVYVVAERDGDRLRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
DB 301 PRALFASRVPRGQRYVYVVAERDGDRLRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
DB 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
DB 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 15
AAB31222
ID AAB31222 standard; protein; 475 AA.

AC AAB31222;

DT 20-APR-2001 (first entry)

DE Amino acid sequence of human sonic hedgehog protein (Shh).

KW Hedgehog related-protein; sonic hedgehog protein; Shh; ischemia; stroke;
KW desert hedgehog protein; Dhh; indian hedgehog protein; Ihh; neuron;
KW neurological condition; nervous system injury; tumour-induced injury;
KW aging; Alzheimer's disease; chronic neurodegenerative disease;
KW parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
KW spinocerebellar degeneration; chronic immunological disease;
KW multiple sclerosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FH

FT Misc-difference 463 /note= "unspecified amino acid encoded by NNN"
FT US6165747-A.
XX 26-DEC-2000.
XX 05-JUN-1995; 95US-00460900.
XX 30-DEC-1993; 93US-00176427.
XX 14-DEC-1994; 94US-00356060.
XX 04-MAY-1995; 95US-00435093.
XX (HARD) HARVARD COLLEGE.
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX Ingham PW, McMahon AP, Tabin CJ, Marti-Gorostiza E, Bumcrot DA;
XX WPI; 2001-079847/09.
XX N-PSDB; AAC87079.
XX Polynucleotides encoding hedgehog proteins, useful for treating diseases
XX of nervous system such as Alzheimer's disease, Parkinson's disease,
XX Huntington's chorea, amyotrophic lateral sclerosis, multiple sclerosis.
XX Claim 10; Col 147-150; 119pp; English.
XX The present sequence represents a hedgehog related-protein. The
XX specification describes a sonic hedgehog protein (Shh), a desert hedgehog
XX protein (Dhh), and an indian hedgehog protein (Ihh). The hedgehog
XX polynucleotides are useful in diagnostic, in antisense therapy and in
XX therapeutic assays for detecting and treating disorders involving, e.g.,
XX aberrant expression of vertebrate hedgehog homologue. Hedgehog
XX polypeptides are useful therapeutically to enhance survival of neurons
XX and other neuron cells and in treating neurological conditions deriving
XX from acute, subacute, or chronic injury to the nervous system, including
XX traumatic injury, chemical injury, vascular injury and deficits (such as the
XX ischemia resulting from stroke), together with infectious/inflammatory
XX and induced-induced injury, aging of the nervous system including
XX Alzheimer's disease, chronic neurodegenerative diseases of the nervous
XX system, including Parkinson's disease, Huntington's chorea, amyotrophic
XX lateral sclerosis, spinocerebellar degenerations, and chronic
XX immunological diseases of the nervous system or affecting the nervous
XX system, including multiple sclerosis
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
DB 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
DB 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
DB 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
DB 181 IHCSVKAENSVAAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
DB 241 FLDRDDGAKKVFYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQRYVYVVAERDGDRLRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVPGQVVVVAERDGDRLLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGAREGA 475

RESULT 16
ABB79137
ID ABB79137 standard; protein; 475 AA.
AC ABB79137;
XX
DT 06-AUG-2002 (first entry)
DE Human sonic hedgehog (Shh) protein SEQ ID NO:13.
XX
KW Sonic hedgehog; Shh; desert hedgehog; Dhh; Indian hedgehog; Ihh;
KW antiparkinsonian; antiarrhythmic; neuroprotective; anticonvulsant;
KW cytosolic; nootropic; spermatogenesis; peripheral nervous system;
KW central nervous system; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; arrhythmia; nerve degeneration; multiple sclerosis;
KW immunological disorder; neoplastic; hyperplastic..
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 463
FT /label= unknown
FT /note= "encoded by NNN"
XX
PN US6384192-B1.
XX
PD 07-MAY-2002.
XX
PF 20-OCT-1997; 97US-00957874.
XX
PR 30-DEC-1993; 93US-00176427.
PR 14-DEC-1994; 94US-00356060.
PR 04-MAY-1995; 95US-00435093.
PR 05-JUN-1995; 95US-00462386.
XX

PA (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
PI Ingham PW, McMahon AP, Tabin CJ;
XX
DR WPI; 2002-442817/47.
DR N-PSDB; ABN87549.
XX
PT New vertebrate hedgehog-related proteins, useful e.g. for promoting
PT differentiation, survival and proliferation of cells, e.g. for treating
PT neurodegeneration.
XX
PS Claim 2; Col 149-152; 116pp; English.
XX
CC The present invention describes an isolated and/or recombinant
CC polypeptide (I) comprising a hedgehog (hh) amino acid (aa) sequence
CC encoded by a nucleic acid (II) that hybridizes under stringent conditions
CC to 1 of 6 sequences (see ABN87544, and ABN87546 to ABN87550). (I) binds
CC to a natural patched receptor. Specifically claimed example of (I) are
CC given in ABB79132 and ABB79134 to ABB79138. (I) has antiparkinsonian,
CC nootropic, neuroprotective, anticonvulsant, antiarrhythmic and cytostatic
CC activities. (I) induces the expression of the BMP-2 and -4 genes, and of
CC the Hoxd gene. (I) can be used: (i) to promote differentiation of
CC neuronal cells and survival of the differentiated cells, specifically
CC dopaminergic or motor neurons, proliferation of chondrocytes, and
CC proliferation, differentiation and/or survival of mesodermal or
CC ectodermal cells, either in cell cultures (particularly for preparation

CC of transplants) or therapeutically; (ii) for detecting loss of response,
CC in tissues or cells, to hh proteins; (iii) in drug screening (to identify
CC (ant)agonists, useful e.g. for inhibition of spermatogenesis); and (iv)
CC for isolation of cognate receptors. (I) may be used therapeutically to
CC treat e.g. injuries/defects in the central or peripheral nervous systems,
CC including Alzheimer's, Parkinson's and Huntington's diseases, or
CC arrhythmias caused by nerve degeneration; immunological disorders of the
CC nervous system, e.g. multiple sclerosis; neoplastic and hyperplastic
CC alterations in the central nervous system, also to promote attachment of
CC prostheses. The present sequence represents the human sonic hedgehog
CC (Shh) protein given in the present invention
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 5; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTILGASG 60
Db 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAISVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAISVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDEGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFCSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFCSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
QY 301 PRALFASRVPGQVVVVAERDGDRLLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQVVVVAERDGDRLLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGAREGA 475

RESULT 17
AAE14297
ID AAE14297 standard; protein; 475 AA.
XX
AC AAE14297;
XX
DT 07-MAR-2002 (first entry)
XX
DE Human Sonic hedgehog (Shh) protein.
XX
KW Neuronal degeneration; hedgehog therapeutic; neurotrophic factor;
KW therapy; amelioration; Alzheimer's disease; Parkinson's disease;
KW Huntington's chorea; amyotrophic lateral sclerosis; schizophrenia;
KW neurological disorder; hypoglycaemia; senile dementia; depression;
KW Korsakoff's disease; acquired immune deficiency syndrome; hypoxia;
KW AIDS dementia; epileptic seizure; Tourette's syndrome; ischaemia;
KW suffocation; neurotoxic injury; cerebrovascular accident; anoxia; trauma;
KW myocardial infarct; drowning; perinatal asphyxia; surgery;
KW drug addiction; stroke; human; Sonic hedgehog; Shh protein; ALS.
XX
OS Homo sapiens.
XX

XX SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 5; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGLGASG 60
Dy 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGLGASG 60

Qy 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQCKDKLNALAISVMNQWPGV 120
Dy 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQCKDKLNALAISVMNQWPGV 120

Qy 121 KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Dy 121 KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

Qy 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Dy 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Qy 241 FLDRDDGAKKVFIYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Dy 241 FLDRDDGAKKVFIYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Qy 301 PRALFASRVRPQGRVYVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Dy 301 PRALFASRVRPQGRVYVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVIEHSHWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPAGA 420
Dy 361 ASCYAVIEHSHWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPAGA 420

Qy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Dy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 19
AAU99483
ID AAU99483 standard; protein; 475 AA.
XX AC AAU99483;
XX DT 07-OCT-2002 (first entry)
XX DE Human sonic hedgehog (Shh) protein.
XX KW Basal cell carcinoma; BCC; non-cancerous skin sample; dermis; epidermis;
XX KW culture medium; hedgehog signalling pathway; growth; development;
XX KW abnormality; cancer; cytostatic; human; Shh; sonic hedgehog.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 463 /label= Unknown
XX FT
XX FN WO200244344-A2.
XX PD
XX PD 06-JUN-2002.
XX PF 28-NOV-2001; 2001WO-US044457.
XX PR 28-NOV-2000; 2000US-0253660P.
XX PA (CURI-) CURIS INC.
XX PI Berg AP, Pepicelli C, Wang F;
XX DR WPI; 2002-557537/59.

DR N-PSDB; ABK88636.
XX
PT Preparing basal cell carcinoma culture useful for identifying BCC
PT therapeutics by contacting non-cancerous skin sample having dermis and
PT epidermis, with culture medium having hedgehog agonist and/or hedgehog
PT protein.
XX
PS Disclosure; Page 107-108; 117pp; English.
XX
CC The present invention relates to methods for preparing basal cell
CC carcinoma (BCC) cultures. The method involves obtaining a non-cancerous
CC skin sample comprising dermis and epidermis and placing it in contact
CC with culture medium comprising a hedgehog agonist and/or hedgehog
CC protein. The method optionally involves either obtaining a BCC sample and
CC placing it in close proximity to a dermis sample, or obtaining a BCC and
CC culturing the BCC sample at a liquid/air interface. The BCC cultures and
CC the methods of the invention are useful for identifying a BCC therapeutic
CC (e.g. a hedgehog agonist or antagonist) and allowing more extensive in
CC vitro studies of BCCs. Since BCC characteristics depend heavily upon
CC hedgehog pathway activity, BCC cultures may be used to identify compounds
CC that regulate the hedgehog signalling pathway. Compounds that affect BCC
CC growth and development may also be useful in treating a wide range of
CC diseases, disorders and abnormalities. The cultures may be used to
CC examine essentially any aspect of BCC biology in vitro, thus leading to
CC the discovery of valuable new therapeutics for treatment of this most
CC common form of cancer. The present sequence represents human sonic
CC hedgehog (Shh) protein
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 5; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGLGASG 60
Dy 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTGLGASG 60

Qy 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQCKDKLNALAISVMNQWPGV 120
Dy 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQCKDKLNALAISVMNQWPGV 120

Qy 121 KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Dy 121 KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

Qy 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Dy 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Qy 241 FLDRDDGAKKVFIYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Dy 241 FLDRDDGAKKVFIYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Qy 301 PRALFASRVRPQGRVYVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Dy 301 PRALFASRVRPQGRVYVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVIEHSHWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPAGA 420
Dy 361 ASCYAVIEHSHWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPAGA 420

Qy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Dy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 20
ADA26256
ID ADA26256 standard; protein; 475 AA.
XX AC ADA26256;
XX DR

DT 20-NOV-2003 (first entry)
XX Human Sonic hedgehog (Shh) polypeptide.
DE
XX
KW Human; Sonic hedgehog; Shh; neuronal cell; skeletogenesis;
KW chondrogenesis; osteogenesis; degenerative disorder; nervous system;
KW neuronal cell death; neural cell; neuromuscular disorder;
KW autonomic disorder; central nervous system disorder; anoxia; ischaemia;
KW peripheral nervous system disorder; tachycardia;
KW atrial cardiac arrhythmia; striated heart; stem cell development;
KW digestive tract; liver; multiple sclerosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 463
FT /label= unknown
XX
XX US2003054437-A1.
XX
XX 20-MAR-2003.
XX
XX 20-OCT-1997; 97US-00954771.
XX
XX 30-DEC-1993; 93US-00176427.
XX 14-DEC-1994; 94US-00356060.
XX 04-MAY-1995; 95US-00435093.
XX 05-JUN-1995; 95US-00462386.
XX
XX (INGH/) INGHAM P W.
XX (MCMA/) MCMAHON A P.
XX (TABI/) TABIN C J.
XX
XX Ingham PW, McMahon AP, Tabin CJ;
XX WPI; 2003-555377/52.
XX N-PSDB; ADA26295.
XX
XX Modulating growth, differentiation or survival of a cell, useful for
XX treating a degenerative disorder of the nervous system characterized by
XX neuronal cell death, comprises contacting the cell with a hedgehog
XX polypeptide.
XX
XX Claim 5; Page 81-82; 121pp; English.
XX
XX The invention relates to a method for modulating growth, differentiation
XX or survival of a cell, comprising contacting the cell with a hedgehog
XX polypeptide. The invention also relates to methods for inducing a cell to
XX differentiate to a neuronal cell phenotype comprising contacting the cell
XX with a hedgehog polypeptide, modulating skeletogenesis by contacting a
XX target tissue of a hedgehog polypeptide to cause chondrogenesis and/or
XX osteogenesis in the target tissue and treating a degenerative disorder of
XX the nervous system characterised by neuronal cell death, comprising
XX administering a hedgehog polypeptide causing prolonged survival of neural
XX cells in the patient, relative to the absence of hedgehog treatment. The
XX hedgehog polypeptides are useful for treating a degenerative disorder of
XX the nervous system characterised by neuronal cell death, including
XX neuromuscular, autonomic or central nervous system disorders,
XX specifically Alzheimer's disease, Parkinson's disease, amyotrophic
XX lateral sclerosis, Pick's disease, Huntington's disease, multiple
XX sclerosis, neuronal damage resulting from anoxia, ischaemia or trauma and
XX neuronal degeneration associated with a natural aging process. The
XX polypeptides may also be used for treating peripheral nervous system
XX disorders including disorders affecting innervation of smooth muscle and
XX endocrine tissue, such as tachycardia or atrial cardiac arrhythmias which
XX may arise from a degenerative condition whereby the nerves innervate the
XX striated muscle of the heart, in nerve prostheses for repairing central
XX and peripheral nerve damage, for treating neoplastic or hyperplastic
XX transformations and in controlling the development of stem cells
XX responsible for the formation of the digestive tract, liver and other
XX organs. This sequence represents the human Sonic hedgehog (Shh)
XX polypeptide.

SQ Sequence 475 AA;
Query Match 99.9%; Score 2467; DB 6; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
DB 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQCKDKLNALAISVMNQPGV 120
DB 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQCKDKLNALAISVMNQPGV 120
QY 121 KLRVTEGWDEGDHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYYESKAH 180
DB 121 KLRVTEGWDEGDHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFCPSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
DB 181 IHCSVKAENSVAAKSGGCGFCPSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVYFVIETREPRERLLLTAAHLLFVAPHNDSATGPEASSGSGPPSGGALG 300
DB 241 FLDRDDGAKKVYFVIETREPRERLLLTAAHLLFVAPHNDSATGPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPCQORVYVVAERDGDRLLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
DB 301 PRALFASRVPCQORVYVVAERDGDRLLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGGDRGGGRVALTAPGA 420
DB 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475
DB 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 21
ADD25260
ID ADD25260 standard; protein; 475 AA.
XX
AC ADD25260;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human Sonic hedgehog (SHH) polypeptide.
XX
KW human; Sonic hedgehog; SHH; patched receptor; spermatogenesis inhibition;
KW ovary function inhibition; embryogenesis;
KW differential tissue maintenance.
XX
OS Homo sapiens.
XX
PN US6576237-B1.
XX
PD 10-JUN-2003.
XX
XX 16-AUG-2000; 2000US-00639695.
PF
XX 30-DEC-1993; 93US-00176427.
PR 14-DEC-1994; 94US-00356060.
PR 04-MAY-1995; 95US-00435093.
PR 05-JUN-1995; 95US-00460900.
XX
XX (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
XX Ingham PW, McMahon AP, Tabin CJ, Bumcrot DA, Marti-Gorostiza E;
XX WPI; 2003-799823/75.
DR N-PSDB; ADD25315.
DR

XX Novel isolated antibody which is immunoreactive with a vertebrate
PT hedgehog protein sequence that binds with patched receptor, useful for
PT blocking action of naturally occurring hedgehog protein, and for
PT inhibiting spermatogenesis.
XX
PS Claim 6; SEQ ID NO 13; 120pp; English.
XX
CC The invention relates to an isolated antibody (I) which is immunoreactive
CC with a hedgehog polypeptide (II) that binds to a patched receptor, where
CC (II) is encoded by nucleic acid which hybridise to a fully defined
CC vertebrate hedgehog (hh) protein. (I) is useful as a hedgehog antagonist
CC by blocking action of naturally occurring hedgehog protein, and therefore
CC for inhibiting spermatogenesis. (I) is also useful for inhibiting normal
CC ovarian function. (I) is useful for blocking the action of one or more
CC hedgehog proteins and allows the study of the role of these proteins
CC e.g., embryogenesis and/or maintenance of differential tissue. (I) is
CC also useful in immunohistochemical staining of tissue samples in order to
CC evaluate the abundance and pattern of expression of the hedgehog
CC polypeptides. (I) is also useful diagnostically in immunoprecipitation
CC and immunoblotting to detect and evaluate hedgehog protein levels as a
CC part of clinical testing procedure. The present sequence represents the
CC amino acid sequence of a hedgehog polypeptide.
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 7; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60

Qy 61 RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120

Qy 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

Qy 181 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Qy 241 FLDRDDGAKKVFYIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Qy 301 PRALFASRVPRGQRYVYVAERDGRRLPAAVHSVTLSBEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQRYVYVAERDGRRLPAAVHSVTLSBEAAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVIEHNSWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHNSWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420

Qy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSSXSRGAGGGAREGA 475

RESULT 22
ABW00868
ID ABW00868 standard; protein; 475 AA.
XX
AC ABW00868;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human sonic hedgehog protein.
XX

KW Human; cell differentiation; Desert hedgehog; Dhh; Sonic hedgehog; shh;
KW Indian hedgehog; Ihh; skeletogenesis; degenerative disorder; ischaemia;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW Huntington's disease; multiple sclerosis; Pick's disease; aging process;
KW trauma; anoxia; antisense gene therapy; neuroprotective; anticonvulsant;
KW nootropic.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Misc-difference 463
FT /note= "Encoded by NNN"
XX
PN US2003186357-A1.
XX
PD 02-OCT-2003.
XX
PF 05-JUN-1995; 95US-00462386.
XX
PR 30-DEC-1993; 93US-00176427.
PR 14-DEC-1994; 94US-00356060.
PR 04-MAY-1995; 95US-00435093.
XX
PA (INGH/) INGHAM P W.
PA (MCMA/) MCMAHON A P.
PA (TABI/) TABIN C J.
XX
XX Ingham PW, McMahon AP, Tabin CJ;
PI WPI; 2003-803151/75.
XX N-PSDB; AAD62097.
DR
XX
XX Modulating cell growth, differentiation or survival, for treating
PT neurodegenerative diseases, such as Alzheimer's or Parkinson's disease,
PT comprises contacting the cell with a hedgehog polypeptide.
XX
PS Claim 5; Page 82-83; Opp; English.
XX
CC The present invention relates to a novel method for modulating growth, the
CC differentiation or survival of a cell. The method involves contacting
CC cell with a hedgehog polypeptide such as Desert hedgehog (Dhh), Sonic
CC hedgehog (shh) and Indian hedgehog (Ihh). The method is used to induce a
CC cell to differentiate to a neuronal cell phenotype. It is used to
CC modulate skeletogenesis. The method is used to treat a degenerative
CC disorders of the nervous system such as neuromuscular, autonomic or
CC central nervous system disorders (e.g., Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, Huntington's disease, multiple
CC sclerosis, Pick's disease, neuronal degeneration associated with a
CC natural aging process and neuronal damage resulting from trauma and
CC neuronal damage resulting from anoxia-ischaemia. The invention is also
CC used for antisense gene therapy. The present sequence is human Shh
CC protein
XX
SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 7; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60

Qy 61 RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120

Qy 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

Qy 181 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFFYVIETREPRERILLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 241 FLDRDDGAKKVFFYVIETREPRERILLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVPRGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGA 420

Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 23

ADD71383

ID ADD71383 standard; protein; 475 AA.

XX

AC ADD71383;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human sonic hedgehog (shh).

DE hedgehog polypeptide; tissue array generation; tissue array maintenance;

KW human; sonic hedgehog; shh.

KW

XX Homo sapiens.

OS

XX

PH Key Location/Qualifiers

FT Misc-difference 463 /note= "Unknown"

FT

XX

PN US2003190696-A1.

XX

PD 09-OCT-2003.

XX

PF 13-DEC-2000; 2000US-00736476.

XX

PR 30-DEC-1993; 93US-00176427.

PR 14-DEC-1994; 94US-00356060.

PR 04-MAY-1995; 95US-00435093.

PR 05-JUN-1995; 95US-00460900.

XX

PA (HARD) HARVARD COLLEGE.

XX

XX Ingham PW, McMahon AP, Tabin CJ, Bumcrot DA, Marti-Gorostiza E;

WPI; 2003-831623/77.

DR N-PSDB; ADD71376.

XX

PT New nucleic acid encoding a hedgehog polypeptide having an amino acid

PT sequence identical or homologous to a vertebrate hedgehog protein, useful

PT for generating or maintaining an array of different vertebrate tissue in

PT vitro and in vivo.

XX

PS Claim 12; SEQ ID NO 13; 118pp; English.

XX

XX The invention describes an isolated nucleic acid encoding a hedgehog

CC polypeptide having an amino acid sequence identical or homologous to a

CC vertebrate hedgehog protein or its portion and not identical to a fully

CC defined 471-bp sequence. The nucleic acid is useful for generating and/or

CC maintaining an array of different vertebrate tissue both in vitro and in

CC vivo. This is the amino acid sequence of human sonic hedgehog (shh).

XX

SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 7; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.le-217;

Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVLSLLVCSGLACGPGRGRRHPKLTPLAYKQFIPNVAEKTIGASG 60

Db 1 MLLARCLLLVLSLLVCSGLACGPGRGRRHPKLTPLAYKQFIPNVAEKTIGASG 60

QY 61 RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120

Db 61 RYEGKISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120

QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYVESKAH 180

Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYVESKAH 180

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFFYVIETREPRERILLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 241 FLDRDDGAKKVFFYVIETREPRERILLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVPRGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGA 420

Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 24

AAB85085

ID AAB85085 standard; protein; 462 AA.

XX

AC AAB85085;

XX

DT 22-AUG-2001 (first entry)

XX

DE Human sonic hedgehog (Shh) polypeptide.

XX

KW Insulin; hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh;

KW desert hedgehog; Dhh; diabetes; pancreatic beta-cell; PBC; IDX-1;

KW neogenesis; hyperinsulinemia.

XX

OS Homo sapiens.

XX

PN WO200141786-A1.

XX

PD 14-JUN-2001.

XX

PF 08-DEC-2000; 2000WO-US033575.

XX

PR 10-DEC-1999; 99US-0170282P.

XX

PA (GEO) GEN HOSPITAL CORP.

XX

PI Habener JF, Thomas MK;

XX

DR WPI; 2001-381492/40.

DR N-PSDB; AAF84005.

XX

PT Treating deficiency of insulin, IDX-1 or pancreatic beta cells in a

PT patient by, administering a hedgehog protein, nucleic acid encoding the

PT protein or cells expressing the protein.

XX

PS Disclosure; Fig 1B; 63pp; English.

XX

CC The invention relates to a method of treating deficiency of insulin, that
CC involves administering a hedgehog protein or nucleic acid encoding the
CC hedgehog protein. The hedgehog proteins that can be used in the method
CC are selected from sonic hedgehog (Shh), indian hedgehog (Ihh) and desert
CC hedgehog (Dhh). The method is useful for treating deficiency of insulin
CC in a patient afflicted with diabetes, by stimulating insulin production
CC in pancreatic beta-cells (PBC). It is also used to treat deficiency of IDX
CC -1 in a patient, by stimulating IDX-1 production in PBC. The hedgehog
CC protein is useful for modulating IDX-1 gene expression or its protein in
CC PBC. This is used to treat deficiency of PBC in a patient, by stimulating
CC neogenesis form beta-cell pancreatic ductal precursor cells. Inhibitors
CC of the hedgehog proteins are useful for suppressing secretion of insulin
CC in a patient afflicted with hyperinsulinemia. The present sequence
CC represents a human Shh polypeptide
XX
SQ Sequence 462 AA;

Query Match 97.5%; Score 2407; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.6e-212;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db |||||
1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db |||||
61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db |||||
121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db |||||
181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db |||||
241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQRVVVAERDGRRLPAAVHVSVTLSSEAGAYAPLTAQGTILINRVL 360
Db |||||
301 PRALFASRVPRGQRVVVAERDGRRLPAAVHVSVTLSSEAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPAGA 420
Db |||||
361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPAGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAKSS 462
Db |||||
421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAKSS 462

RESULT 25
ADA09286
ID ADA09286 standard; protein; 462 AA.
XX
AC ADA09286;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human Sonic Hedgehog protein (Shh).
XX
KW Human; hedgehog protein; desert; indian; sonic; Dhh; Ihh; Shh;
KW cytosstatic; gene therapy; carcinogenesis; gastric; colonic; cancer;
KW gastrointestinal tract; colonic adenomatous polyp;
KW invasive adenocarcinoma; intestinal adenoma; desmoid tumour.
XX
OS Homo sapiens.
XX
PN W02003070265-A2.
XX

PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-NL000127.
XX
PR 20-FEB-2002; 2002EP-00075690.
XX
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
XX Van Den Brink GR, Poppelbosch MP, Hardwick JCH, Van Deventer SJH;
PI WPI; 2003-697568/66.
XX
XX Use of a Hedgehog protein for treating Hedgehog protein deficiency in the
PT gastrointestinal tract, or for preventing gastric or colonic cancer,
PT colonic adenomatous polyps, invasive adenocarcinomas, small intestinal
PT adenomas.
XX
XX Disclosure; Page 47-49; 67pp; English.
XX
CC The invention relates to treating a deficiency of a Hedgehog protein in
CC the gastrointestinal (GI) tract. The method of the invention comprises
CC providing a source of Hedgehog protein to the GI tract of a subject
CC suffering from the deficiency of this protein. Hedgehog proteins include
CC Desert (Dhh), Indian (Ihh) and Sonic (Shh). The treatment of the
CC deficiency of a Hedgehog protein in the GI tract is useful for the
CC prophylaxis of carcinogenesis in the GI tract, gastric or colonic cancer,
CC and for the treatment of a GI tract carcinoma, particularly gastric or
CC colonic cancer. The source Hedgehog protein may also be administered to
CC prevent or reverse colonic adenomatous polyps, invasive adenocarcinomas,
CC small intestinal adenomas and cancers, and desmoid tumors. Loss of Indian
CC hedgehog (Ihh) expression was evident in the earliest recognizable stage
CC in the sequence of events that is thought to progress to colon cancer.
CC Ihh was found to be not expressed in malignant colonic epithelial cells.
CC The colon cancer cell HT-29 will only express Ihh protein after
CC differentiation with butyrate. The in vitro differentiation of HT-29
CC cells with recombinant hedgehog (Hh) protein was determined. Forty-eight
CC hour treatment of HT-29 cells induces Willin expression to a similar
CC extent as after treatment with 5 mM butyrate. Data show that exogenous Hh
CC protein was sufficient to restore differentiation of colon carcinoma
CC cells. Hedgehog proteins may also be used in gene therapy techniques. The
CC current sequence represents the human Sonic hedgehog protein (Shh).
XX
SQ Sequence 462 AA;

Query Match 97.5%; Score 2407; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.6e-212;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db |||||
1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db |||||
61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db |||||
121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db |||||
181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db |||||
241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQRVVVAERDGRRLPAAVHVSVTLSSEAGAYAPLTAQGTILINRVL 360
Db |||||
301 PRALFASRVPRGQRVVVAERDGRRLPAAVHVSVTLSSEAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPAGA 420

Db 361 ASYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462
421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462

RESULT 26
AAB85738
ID AAB85738 standard; protein; 463 AA.
XX AAB85738;
AC
XX
DT 29-OCT-2001 (first entry)
XX
DE Human sonic hedgehog (Shh) polypeptide.
XX
DE Hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh; Dhh;
KW desert hedgehog; cell differentiation; human.
XX
XX Homo sapiens.
OS
XX US6271363-B1.
PN
PD 07-AUG-2001.
XX
XX 20-OCT-1997; 97US-00954698.
PF
XX 30-DEC-1993; 93US-00176427.
PR 14-DEC-1994; 94US-00356060.
PR 04-MAY-1995; 95US-00435093.
PR 05-JUN-1995; 95US-00462386.
XX
XX (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
PA
XX
XX Ingham PW, McMahon AP, Tabin CJ;
XX
XX WPI; 2001-456723/49.
DR N-PSDB; AAH76112.
DR
XX Novel nucleic acid encoding a hedgehog polypeptide, used to produce the polypeptide, which is used to promote proliferation, survival, and/or differentiation of neuronal and mesodermal tissue.
PT
XX Claim 1; Col 133-136; 118pp; English.
PS
XX The invention relates to nucleic acids encoding hedgehog proteins selected from sonic hedgehog (Shh), indian hedgehog (Ihh), desert hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the formation of ordered spatial arrangements of differentiated tissue in vertebrates. The nucleic acid sequences are useful for producing hedgehog proteins, used for promoting differentiation of, or survival of differentiated, neuronal cells, and for promoting proliferation, survival or differentiation of mesenchymal, endodermal or ectodermal tissue, particularly chondrocytes, or testicular germ line cells. The present sequence represents a human Shh polypeptide
XX
SQ Sequence 463 AA;

Query Match 97.5%; Score 2407; DB 4; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.7e-212;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Oy 61 RYEGKISRNSERFKELTPNTNPDIIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNTNPDIIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 120

Oy 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYESKAH 180
Oy 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDEFLT 240
Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDEFLT 240
Oy 241 FLDRDDGAKKVYVVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVYVVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Oy 301 PRALFASRVPCQQRVYVVAERDGDRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPCQQRVYVVAERDGDRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
Oy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Oy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462

RESULT 27
AAW48736
ID AAW48736 standard; protein; 462 AA.
XX
AC AAW48736;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human mutated sonic hedgehog (SHH) protein (Met-114Ile).
XX
KW Sonic hedgehog; SHH protein; tumorigenesis; oncogenesis;
KW basal cell carcinoma; breast cancer; medulloblastoma; tumour;
KW cell proliferation; cell differentiation; wound healing; diagnosis;
KW therapy; human.
XX
OS Homo sapiens.
XX
XX WO9821227-A1.
PN
XX 22-MAY-1998.
PD
XX 12-NOV-1997; 97WO-US020227.
PF
XX 13-NOV-1996; 96US-00748591.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Epstein E, Hu Z, Bonifas J;
PI
XX WPI; 1998-297857/26.
XX N-PSDB; AAV18404.
DR
XX New nucleic acid encoding oncogenic human hedgehog protein - useful for, e.g. treatment and diagnosis of cancer and diseases involving cell proliferation or differentiation.
PT
XX Claim 6; Page 32-33; 47pp; English.
PS
XX This human sonic hedgehog (SHH) protein carries a spontaneously occurring mutation (M14I substitution) that is associated with oncogenic transformation of human cells. The amino acid substitution results from a mutation of the SHH gene (see AAV18404). This mutation was identified in a basal cell carcinoma. A second basal cell carcinoma, as well as a medullocarcinoma and a breast cancer were shown to carry an independently arising different mutation (see AAW48735). Purified oncogenic HH proteins, and methods for producing the proteins using mammalian (preferably human) host cells are claimed. The HH proteins can be used: in functional mapping; therapeutically for modulating cell proliferation

CC and differentiation, e.g. in cases of wound healing or any of a very wide
CC range of conditions involving reduced hedgehog signalling such as bone
CC formation, hyperproliferative or hypoproliferative skin disease, growth
CC of hair, neurodegeneration (Alzheimer's disease etc.) or autonomic
CC disorders of the peripheral nervous system, e.g. cardiac arrhythmia; to
CC study physiological pathways; and to screen for drugs that modulate HH
CC activity and expression. HH proteins are also useful in vitro for
CC sustaining reproduction of neural progenitor cells. Detecting presence of
CC oncogenic HH mutations is used to characterise the phenotype of a tumour;
CC similar analyses can be done at the protein level using antibodies, which
CC may also be used to treat human cancers
XX
SQ Sequence 462 AA;

Query Match 97.3%; Score 2403; DB 2; Length 462;
Best Local Similarity 99.8%; Pred. No. 1.5e-211;
Matches 461; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db MLLARCLLLVSSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120

QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

QY 181 IHCSVKAENSVAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db IHCSVKAENSVAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
Db PRALFASRVPGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462

RESULT 28
AAW48735
ID AAW48735 standard; protein; 462 AA.
XX
AC AAW48735;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human mutated sonic hedgehog (SHH) protein (His133-Tyr).
XX
KW Sonic hedgehog; SHH protein; tumorigenesis; oncogenesis;
KW basal cell carcinoma; breast cancer; medulloblastoma; tumour;
KW cell proliferation; cell differentiation; wound healing; diagnosis;
KW therapy; human.
XX
OS Homo sapiens.
XX
PN WO9821227-A1.
XX
PD 22-MAY-1998.
XX
PF 12-NOV-1997; 97WO-US020227.

XX 13-NOV-1996; 96US-00748591.
PR (REGC) UNIV CALIFORNIA.
XX
PA Epstein E, Hu Z, Bonifas J;
XX
PI WPI; 1998-297857/26.
DR N-PSDB; AAV18403.
XX
PT New nucleic acid encoding oncogenic human hedgehog protein - useful for,
PT e.g. treatment and diagnosis of cancer and diseases involving cell
PT proliferation or differentiation.
XX
PS Claim 6; Page 28-29; 47pp; English.
XX
CC This human sonic hedgehog (SHH) protein carries a spontaneously occurring
CC mutation (H133Y substitution) that is associated with oncogenic
CC transformation of human cells. The amino acid substitution results from a
CC mutation of the SHH gene (see AAV18403). This mutation was identified in
CC 3 independently arising tumours (a basal cell carcinoma,
CC medullocarcinoma, and breast cancer). A second basal cell carcinoma was
CC shown to carry a different mutation (see AAW48736). Purified oncogenic HH
CC proteins, and methods for producing the proteins using mammalian
CC (preferably human) host cells are claimed. The HH proteins can be used:
CC in functional mapping; therapeutically for modulating cell proliferation
CC and differentiation, e.g. in cases of wound healing or any of a very wide
CC range of conditions involving reduced hedgehog signalling such as bone
CC formation, hyperproliferative or hypoproliferative skin disease, growth
CC of hair, neurodegeneration (Alzheimer's disease etc.) or autonomic
CC disorders of the peripheral nervous system, e.g. cardiac arrhythmia; to
CC study physiological pathways; and to screen for drugs that modulate HH
CC activity and expression. HH proteins are also useful in vitro for
CC sustaining reproduction of neural progenitor cells. Detecting presence of
CC oncogenic HH mutations is used to characterise the phenotype of a tumour;
CC similar analyses can be done at the protein level using antibodies, which
CC may also be used to treat human cancers
XX

SQ Sequence 462 AA;
Query Match 97.2%; Score 2401; DB 2; Length 462;
Best Local Similarity 99.8%; Pred. No. 2.4e-211;
Matches 461; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db MLLARCLLLVSSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120

QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

QY 181 IHCSVKAENSVAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db IHCSVKAENSVAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
Db PRALFASRVPGQRVVVAERDGDRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGGGRVALTAPGA 420
Db ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462

||||| 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSS 462

Db AAW61488 standard; protein; 437 AA.

AC AAW61488;

XX 25-MAR-2003 (revised)

DT 20-OCT-1998 (first entry)

XX Mouse sonic hedgehog (shh) protein.

DE Hedgehog polypeptide; neuronal cell proliferation; zebrafish; shh;

XX cholesterol biosynthesis; pituitary gland gene expression; mouse;

KW tiggly-winkle hedgehog protein; twhh; sonic hedgehog; major limb trauma;

KW neuronal degeneration; nerve-sparing agent; Smith-Lemli-Optiz syndrome.

XX

OS Mus sp.

XX WO9830576-A1.

PN 16-JUL-1998.

PD 07-OCT-1997; 97WO-US015753.

XX 07-OCT-1996; 96US-00729743.

PR 02-OCT-1997; 97US-0061323P.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PA Beachy'PA, Porter JA;

XX WPI; 1998-399053/34.

DR

XX New hedgehog-derived poly:peptide(s) - used to develop products for

PT modulating proliferation or differentiation of neuronal cells,

PT cholesterol biosynthesis or transport or expression of pituitary gland

PT Gene(s).

XX Claim 13; Page 153-154; 210pp; English.

PS

XX This represents a mouse sonic hedgehog (shh) protein sequence. The

CC invention provides methods and compounds for modulating proliferation or

CC differentiation of neuronal cells, cholesterol biosynthesis or transport

CC or expression of pituitary gland genes. The method for affecting

CC cholesterol biosynthesis or transport in a cell comprises contacting a

CC cell with a compound that affects hedgehog, thereby affecting cholesterol

CC biosynthesis or transport. The methods for inhibiting the neural inducing

CC activity of a hedgehog polypeptide in cells, and for inducing pituitary

CC gland gene expression utilises sequences selected from a zebrafish tiggly-

CC winkle hedgehog (twhh) protein (AAW61485), a zebrafish sonic hedgehog

CC (shh) protein (AAW61486), a chicken shh protein (AAW61487) or a mouse shh

CC protein (AAW61488). The products and methods provide for compounds which

CC can affect hedgehog activity. They can be used for treating disorders

CC which arise from neuronal degeneration or abnormal function. They can

CC also be used as nerve-sparing agents or in restoring or promoting

CC appropriate patterning during the healing of major limb trauma. They can

CC also be used for treating Smith-Lemli-Optiz syndrome. The products can

CC also be used for detection and diagnosis. (Updated on 25-MAR-2003 to

CC correct PA field.)

XX

SQ Sequence 437 AA;

Query Match 83.8%; Score 2068; DB 2; Length 437;

Best Local Similarity 87.4%; Pred. No. 8.3e-181;

Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLIARCLLVLVSSLLVCSGLACGPGRGKRRHPKLLTPLAYKQFIPNVAEKTGLGASG 60

Db 2 LLLIARCLLVILASSLLVCPGLACGPGRGKRRHPKLLTPLAYKQFIPNVAEKTGLGASG 61

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALSAISVMNQWPGV 120

Db :|||||

62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALSAISVMNQWPGV 121

QY 121 KLRVTEGWEDEGHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYVESKAH 180

Db :|||||

122 KLRVTEGWEDEGHSEESLHYEGRAVDITTSDRDRSKYGMRLARLAVEAGFDWVYVESKAH 181

QY 181 IHCSVKAENSVAAKSGGCGPPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db :|||||

182 IHCSVKAENSVAAKSGGCGPPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFFVVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300

Db :|||||

242 FLDRDEGAKKVFFVVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

QY 301 PRALFASRVVRPGQRVVVAERDGDRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db :|||||

287 PSALFASRVVRPGQRVVVAERGGDRRLPAAVHVSVTLREEEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDGGGSGGDRGGGGRVALTAPGA 420

Db :|||||

347 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSS 462

Db :|||||

396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLGMAVKSS 437

RESULT 30

AA885086

ID AA885086 standard; protein; 437 AA.

XX

AC AA885086;

XX

DT 22-AUG-2001 (first entry)

XX Mouse sonic hedgehog (Shh) polypeptide.

DE

XX Insulin; hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh;

KW desert hedgehog; Dhh; diabetes; pancreatic beta-cell; PBC; IDX-1;

KW neogenesis; hyperinsulinemia.

XX

OS Mus musculus.

XX

PN WO200141786-A1.

XX

PD 14-JUN-2001.

XX

PF 08-DEC-2000; 2000WO-US033575.

XX

PR 10-DEC-1999; 99US-0170282P.

XX (GEHO) GEN HOSPITAL CORP.

XX

PI Habener JF, Thomas MK;

XX

DR WPI; 2001-381492/40.

DR N-PSDB; AAF84006.

XX

PT Treating deficiency of insulin, IDX-1 or pancreatic beta cells in a

PT patient by, administering a hedgehog protein, nucleic acid encoding the

PT protein or cells expressing the protein.

XX

PS Disclosure; Fig 2B; 63pp; English.

XX

CC The invention relates to a method of treating deficiency of insulin, that

CC involves administering a hedgehog protein or nucleic acid encoding the

CC hedgehog protein. The hedgehog proteins that can be used in the method

CC are selected from sonic hedgehog (Shh), indian hedgehog (Ihh) and desert

CC hedgehog (Dhh). The method is useful for treating deficiency of insulin

CC in a patient afflicted with diabetes, by stimulating insulin production

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHMPLGMVKSS 437

RESULT 32
AA97559
ID AAY97559 standard; protein; 437 AA.
XX AAY97559;
AC AAY97559;
XX 05-APR-2001 (first entry)
DT Mouse sonic hedgehog protein sequence.

KW Mouse; Hedgehog signalling pathway; inhibitor; autoimmune disorder;
KW epithelial cell hyperplasia; fibrosis; inflammation; adenocarcinoma;
KW immune disorder; cancer; thyroiditis; insulinitis; multiple sclerosis;
KW iridocyclitis; uveitis; orchitis; hepatitis; Addison's disease; asthma;
KW myasthenia gravis; rheumatoid arthritis; lupus erythematosus; emphysema;
KW adult respiratory distress syndrome; chronic bronchitis; atelectasis;
KW silicosis; hypersensitivity pneumonitis; idiopathic pulmonary fibrosis;
KW pneumonia; pleural fibrosis; atherosclerosis; myocardial infarction;
KW gastrointestinal tract disorder; hepatic disease; Alzheimer's disease;
KW Wnt signalling pathway; BMP signalling pathway; sonic hedgehog; SHH.
XX Mus musculus.
OS
XX WO200074706-A1.
XX 14-DEC-2000.
XX 05-JUN-2000; 2000WO-GB002191.
PF 08-JUN-1999; 99GB-00013350.
PR 16-SEP-1999; 99GB-00021953.
XX (LORA-) LORANTIS LTD.
XX Lamb JR, Hoyne GF, Dallman MJ;
PI
XX WPI; 2001-061652/07.
DR N-PSDB; AAA37897.
XX Use of an inhibitor of a Hedgehog signaling pathway in preparation of a
PT medicament for treating epithelial cell hyperplasia, inflammation, cancer
PT or an immune disorder.
XX Disclosure; Page 70; 78pp; English.

XX This sequence is mouse sonic hedgehog (SHH), and is part of the Hedgehog
CC signalling pathway. The invention relates to the use of an inhibitor of a
CC Hedgehog signalling pathway, or an inhibitor of a target pathway of the
CC hedgehog signalling pathway, in the preparation of a medicament for
CC treating epithelial cell hyperplasia, fibrosis of tissue, inflammation,
CC cancer (especially adenocarcinoma) or an immune disorder. The immune
CC disorder can be an autoimmune disorder such as thyroiditis, insulinitis,
CC multiple sclerosis, iridocyclitis, uveitis, orchitis, hepatitis,
CC Addison's disease, myasthenia gravis, rheumatoid arthritis or lupus
CC erythematosus. Medicament containing the inhibitors is also useful for
CC treating lung or kidney diseases such as adult respiratory distress
CC syndrome, chronic obstructive airway disorders including asthma,
CC emphysema and chronic bronchitis, atelectasis, occupational lung disease
CC including silicosis, hypersensitivity diseases of lung such as
CC hypersensitivity pneumonitis, idiopathic interstitial lung diseases such
CC as idiopathic pulmonary fibrosis, pneumonia including interstitial
CC pneumonia, desquamative interstitial pneumonia and acute interstitial
CC pneumonia, and pleural fibrosis. They can also be used in the treatment
CC of inflammation associated with atherosclerosis, e.g. myocardial
CC infarction, diseases of the gastrointestinal tract, hepatic diseases and
CC diseases of the central nervous system e.g. Alzheimer's disease. The
CC hedgehog signalling pathway is that of Sonic hedgehog, Indian hedgehog or

CC Desert hedgehog, the target pathway of the hedgehog signalling pathway is
CC Wnt or BMP signalling pathway
XX
SQ Sequence 437 AA;

Query Match 83.8%; Score 2068; DB 4; Length 437;
Best Local Similarity 87.4%; Pred. No. 8.3e-181;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQIFPNAEKTLGASG 60
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 61
2 LLLARCLVILASSLLVCPGLACGPGRGFKRRHPKLTPLAYKQIFPNAEKTLGASG 61

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTORCKLNALAI SVMNQPGV 120
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 121
62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTORCKLNALAI SVMNQPGV 121

QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 181
122 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 181

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 241
182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVVIETREPRERLLTLTAHLLFVAPHNDSATGEPPEASSGSGPPSGGALG 300
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 306
242 FLDRDEGAKKVFYVVIETLEPRERLLTLTAHLLFVAPHND-----SGTPG 286

QY 301 PRALFASRVRCQORVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQTILINRVL 360
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 366
287 PSALFASRVRCQORVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQTILINRVL 366

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGGGRVALTAPGA 420
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 426
347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db :|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 468
396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHMPLGMVKSS 437

RESULT 33
AA021264
ID AAO21264 standard; protein; 437 AA.
XX
AC AAO21264;
XX
DT 05-AUG-2002 (first entry)
XX
DE 437-mer wild-type sonic hedgehog protein.
XX
KW Sonic hedgehog protein; amino terminal protein; modulate differentiation;
KW signalling developmental process; neural plate; ligand; patched receptor;
KW wild-type.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Cleavage-site 198..200
FT /label= GCF autoprocessing site
FT /note= "This is an autoproteolytic site. Cleavage occurs
FT between the Gly-Cys residues"
XX
PN WO200224151-A2.
XX
XX 28-MAR-2002.
XX
XX 24-SEP-2001; 2001WO-US042438.
XX
XX 22-SEP-2000; 2000US-0235153P.
XX
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA

XX
PI Beachy PA;
XX
DR WPI; 2002-425894/45.
XX
PT New isolated Sonic hedgehog amino terminal protein which is involved in a
PT signaling developmental process, useful for identifying compounds that
PT modulate differentiation of neural plate cells.
XX
PS Claim 1; Fig 4; 50pp; English.
XX
CC The invention relates to an isolated protein having the amino acid
CC sequence of a Sonic hedgehog amino terminal protein (involved in
CC signalling developmental process), where alanine is substituted for amino
CC acid residues at a position such as 51, 52, 56, 75, 90, 76, 81, 105, 116,
CC 132, 135, 138, 168, 177, 189 or 195 or their combination, where the
CC sequence listing of the terminal protein is not given in specification.
CC The invention generally relates to methods for identifying compounds that
CC modulate differentiation of neural plates using hedgehog proteins as
CC ligands for the patched receptor. This sequence represents the 437-mer
CC wild-type sonic hedgehog protein of the invention
XX
SQ Sequence 437 AA;

Query Match 83.8%; Score 2068; DB 5; Length 437;
Best Local Similarity 87.4%; Pred. No. 8.3e-181;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 61
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 121
QY 121 KLRVTEGWDEDDGHSEESLHYEGRVAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db 122 KLRVTEGWDEDDGHSEESLHYEGRVAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 181
QY 181 IHCSVKAENSVAAKSGCGFCPSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGCGFCPSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPGQRVYVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQFTILINRVL 360
Db 287 PSALFASRVPGQRVYVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTPGA 420
Db 347 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHICTWLLDSETMHPGLGVAVKSS 437

RESULT 34
ABG71358
ID ABG71358 standard; protein; 437 AA.
XX
AC ABG71358;
XX
DT 23-JAN-2003 (first entry)
XX
DE Mouse sonic hedgehog (SHH) polypeptide.
XX
KW Mouse; Hedgehog signalling pathway; T-cell mediated disease;
KW T-cell apoptosis; Notch signalling pathway; cancer; breast; prostate;

KW ovary; T-cell activation; T-cell proliferation; lymphoma; carcinoma;
KW autoimmune disease; inflammatory disease; proliferative disorder;
KW viral infection; genetic immunodeficiency; neurodegenerative disease;
KW myelodysplastic syndrome; ischaemic injury; toxin-induced disease;
KW wasting disease; sonic hedgehog; SHH.
XX
OS Mus musculus.
XX
FN WO200280952-A2.
XX
PD 17-OCT-2002.
XX
XX 09-APR-2002; 2002WO-GB001666.
PF
XX 09-APR-2001; 2001GB-00008872.
PR
XX 09-APR-2001; 2001GB-00008873.
XX
FA (LORA-) LORANTIS LTD.
PI Lamb JR, Hoyne GF, Dallman MJ, Champion BR;
XX
XX WPI; 2003-058470/05.
DR N-PSDB; ABS55983.
XX
PT Use of a modulator of Hedgehog signaling pathways for treating T-cell
PT mediated disease or infection and diseases associated with increased or
PT decreased T-cell apoptosis and T-cell proliferation.
XX
PS Disclosure; Page 149; 154pp; English.
XX
CC The invention relates to use of a modulator of a Hedgehog signalling
CC pathway or a modulator of a target of the pathway in the preparation of a
CC medicament for treating T-cell mediated disease or infection or a disease
CC or disorder associated with increased or decreased T-cell apoptosis and
CC for modification of (peripheral) T-cell activation or proliferation or T-
CC cell apoptosis, and for modulation of the Notch signalling pathway in
CC immune cells. The modulator is useful for treating cancer of the breast,
CC prostate or ovary, lymphomas and carcinomas, autoimmune diseases such as
CC systemic lupus erythematosus, multiple sclerosis and diabetes,
CC inflammatory diseases such as osteoarthritis and Crohn's disease.
CC proliferative disorders such as atherosclerosis and psoriasis, viral
CC infections such as AIDS and herpesviruses, genetic immunodeficiencies,
CC neurodegenerative diseases such as Alzheimer's disease and Parkinson's
CC disease, myelodysplastic syndromes such as aplastic anaemia, ischaemic
CC injuries such as myocardial infarction, toxin-induced diseases such as
CC cirrhosis and wasting diseases such as cachexia. This sequence represents
CC the mouse sonic hedgehog (SHH) protein
XX
SQ Sequence 437 AA;

Query Match 83.8%; Score 2068; DB 6; Length 437;
Best Local Similarity 87.4%; Pred. No. 8.3e-181;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 61
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 121
QY 121 KLRVTEGWDEDDGHSEESLHYEGRVAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db 122 KLRVTEGWDEDDGHSEESLHYEGRVAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 181
QY 181 IHCSVKAENSVAAKSGCGFCPSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGCGFCPSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

Db 242 FLDRDEGAKKVYFVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

Qy 301 PRALFASRVRPQQRVYVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVRPQQRVYVVAERGDRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346

Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGSDSGGDRGGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395

Qy 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHMPLGMVKSS 437

RESULT 38

AAW97768

ID AAW97768 standard; protein; 437 AA.

XX

AC AAW97768;

DT 21-MAY-1999 (first entry)

XX Mouse Sonic hedgehog (Shh) protein.

DE Sonic hedgehog; Shh protein; mouse; dopaminergic; GABA-nergic;

XX ptc therapeutic; patched; signal transduction; Parkinson's disease;

KW Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia;

KW hypoxia; neuroprotective; therapy.

XX

OS Mus sp.

XX

PN WO9904775-A2.

XX

PD 04-FEB-1999.

XX

PF 24-JUL-1998; 98WO-US015419.

XX

PR 24-JUL-1997; 97US-00900220.

XX

PA (ONTO-) ONTOGENY INC.

XX

PI Miao N, Wang M, Mahanthappa NK, Pang K;

XX

DR WPI; 1999-142578/12.

DR N-PSDB; AAX07274.

XX

PT Increasing the survival of neuronal, dopaminergic and GABA-nergic cells -

PT by using a ptc therapeutic such as a protein kinase inhibitor, or an

PT agent derived from hedgehog polypeptides, useful in the treatment of

PT Parkinson's disease.

XX

PS Disclosure; Page 89-91; 138pp; English.

XX

This polypeptide is mouse Shh Sonic hedgehog protein. The invention is based on the finding that hedgehog proteins are useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra. Exemplary disorders include Parkinson's disease, Huntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs encoding recombinant hedgehog polypeptides and trans-activation constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human ihh and Dhh polypeptides (see AAW97763-64) are preferred. The products can also be used for the maintenance of such neuronal cells in cultures, and to enhance the implantation of such neuronal cells in an animal. They can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent

XX Sequence 437 AA;

SQ

Query Match 83.6%; Score 2065; DB 2; Length 437;

Best Local Similarity 87.2%; Pred. No. 1.6e-180;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLCASG 60

Db 2 LLLARCLVLILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLCASG 61

Qy 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV 120

Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV 121

Qy 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRRSKYGLARLAVEAGFDWVYYESKAH 180

Db 122 RLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRRSKYGLARLAVEAGFDWVYYESKAH 181

Qy 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241

Qy 241 FLDRDDGAKKVYFVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 242 FLDRDEGAKKVYFVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

Qy 301 PRALFASRVRPQQRVYVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVRPQQRVYVVAERGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346

Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGSDSGGDRGGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395

Qy 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHMPLGMVKSS 437

RESULT 39

AAW05513

ID AAW05513 standard; protein; 437 AA.

XX

AC AAW05513;

XX

DT 05-JUL-1999 (first entry)

XX

DE Mouse Sonic hedgehog protein Shh.

XX

KW Sonic hedgehog; Shh protein; mouse; hedgehog therapeutic;

KW ptc therapeutic; patched; signal transduction; muscle atrophy; cachexia;

KW muscular myopathy; myoblastic sarcoma; therapy.

XX

OS Mus sp.

XX

PN WO9910004-A2.

XX

PD 04-MAR-1999.

XX

PF 28-AUG-1998; 98WO-US017922.

XX

PR 29-AUG-1997; 97US-0057394P.

XX

PA (ONTO-) ONTOGENY INC.

XX

PI Bladgen CS, Currie PD, Ingham PW, Hughes SM;

XX

DR WPI; 1999-243557/20.

DR N-PSDB; AAX25101.

XX

PT A new method to regulate muscle growth.

XX

| | | |
|----|---|----------|
| PS | Disclosure; Page 115-116; 130pp; English. | |
| XX | The present sequence is mouse Sonic hedgehog protein Shh. The invention | |
| CC | relates to a method for modulating the formation and/or maintenance of | |
| CC | muscle tissue by ecotopically contacting muscle cells, especially muscle | |
| CC | stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic | |
| CC | (i.e. hedgehog polypeptides and gene therapy constructs) or ptc | |
| CC | therapeutic (i.e. a small organic molecule that mimics the effect of | |
| CC | hedgehog proteins on patched signalling, or activators or potentiates | |
| CC | patched signalling) in an amount effective to alter the growth state of | |
| CC | the treated cells. Also claimed is a method for treatment or prevention | |
| CC | of disorders of, or surgical or cosmetic repair of, such muscle tissues, | |
| CC | by administering a hedgehog polypeptide or ptc therapeutic. The disorder | |
| CC | may be muscle atrophy, in particular skeletal muscle atrophy or cardiac | |
| CC | muscle atrophy, cachexia, or muscular myopathy (all claimed). The | |
| CC | hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic- | |
| CC | derived tissue to provide treatment of hyperblastic or neoplastic growth | |
| CC | of muscle tissue such as in myoblastic sarcoma (also claimed). The | |
| CC | hedgehog therapeutic preferably comprises at least a bioactive | |
| CC | extracellular portion of a hedgehog protein (see AAY05510-19) encoded by | |
| CC | a vertebrate hedgehog gene (see AAX25098-107), especially a human | |
| XX | hedgehog gene | |
| SQ | Sequence 437 AA; | |
| | Query Match 83.6%; Score 2065; DB 2; Length 437; | |
| | Best Local Similarity 87.2%; Pred. No. 1.6e-180; | |
| | Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3; | |
| QY | 1 MLLARCLLLVSVSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLGASG 60 | |
| Db | 2 LLLARCFVLVILASSLLVCPGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLGASG 61 | |
| QY | 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 120 | |
| Db | 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 121 | |
| QY | 121 KLRVTEGWDEGDHSESLHYEGRAVDITTSRDRSKYGLMARLAVEAGFDWVYVESKAH 180 | |
| Db | 122 RLRVTEGWDEGDHSESLHYEGRAVDITTSRDRSKYGLMARLAVEAGFDWVYVESKAH 181 | |
| QY | 181 IHCSVKAENSVAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240 | |
| Db | 182 IHCSVKAENSVAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241 | |
| QY | 241 FLDRDDGAKKVFIYIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300 | |
| Db | 242 FLDRDEGAKKVFIYIETLEPRERLLTAAHLLFVAPHND-----SGPTPG 286 | |
| QY | 301 PRALFASRVPGQRYVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360 | |
| Db | 287 PSALFASRVPGQRYVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAHGTILINRVL 346 | |
| QY | 361 ASCYAVIEHSHWAHRAFPFLAHALLAALAPARTDRGDSGGDRGGGGRRVALTAPGA 420 | |
| Db | 347 ASCYAVIEHSHWAHRAFPFLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395 | |
| QY | 421 ADAPGAGATAGIHWYSQLLYQIGTWLIDSEALHPLGMVAVKSS 462 | |
| Db | 396 TEARGAEPTAGIHWYSQLLYHIGTWLIDSETMHPPLGMVAVKSS 437 | |
| | RESULT 40 | |
| AA | AY96246 | |
| ID | AA96246 standard; protein; 437 AA. | |
| XX | AC | AY96246; |
| XX | XX | |
| DT | 11-SEP-2000 (first entry) | |
| XX | XX | |
| DE | Partial mouse Shh. | |
| XX | XX | |
| KW | Mouse; sonic hedgehog; Shh; neuromuscular disorder; neuropathy; | |
| KW | Guillain-Barre syndrome; peripheral neuropathy; diabetes; alcoholism; | |
| KW | chronic inflammatory demyelinating polyneuropathy; CIPD; gene therapy; | |
| KW | infection; inflammation; hereditary neuropathy; | |
| KW | Charcot-Marie-Tooth disease; vasculitis; lung cancer; tumour; | |
| KW | multiple myeloma; nutritional imbalance; kidney disease; | |
| KW | hypothyroid neuropathy; trauma; Refsum's disease; Abetalipoproteinemia; | |
| KW | Tangier disease; Krabbe's disease; Metachromatic leukodystrophy; | |
| KW | Fabry's disease; CMT; GBS; Dejerine-Sottas syndrome; acute neuropathy; | |
| KW | Amyotrophic lateral sclerosis; ALS; Miller-Fisher syndrome; amyloidosis; | |
| KW | Hereditary sensory neuropathy Type II; HSN II; B-cell lymphoma; | |
| KW | Waldenstrom's Macroglobulaemia; Chronic lymphocytic Leukaemia; | |
| XX | neuroprotective; cytoprotective; patched-mediated signal transduction. | |
| OS | Mus sp. | |
| XX | WO200027422-A2. | |
| PN | 18-MAY-2000. | |
| XX | | |
| PD | | |
| XX | | |
| PF | 08-NOV-1999; 99WO-US026334. | |
| XX | | |
| PR | 06-NOV-1998; 98US-00187387. | |
| XX | | |
| PA | (BIOJ) BIOGEN INC. | |
| PA | (ONTO-) ONTOGENY INC. | |
| XX | Galdes A, Mahanthappa N; | |
| PI | | |
| XX | WPI; 2000-387341/33. | |
| DR | N-PSDB; AAA30277. | |
| XX | | |
| PT | Novel method of preventing deterioration of peripheral nerves, useful for | |
| PT | treating or preventing neuropathy, e.g. where associated with diabetes or | |
| PT | viral infection, by administering hedgehog or patched agent. | |
| XX | | |
| PS | Claim 7; Page 131-132; 152pp; English. | |
| XX | | |
| CC | The present sequence is the partial mouse sonic hedgehog protein, Shh. | |
| CC | This sequence inhibits expression of the patched gene which has been | |
| CC | implicated in neuromuscular disorders (neuropathies). This sequence may | |
| CC | therefore be used for treating neuromuscular disorders i.e. preventing | |
| CC | degradation in function of motor or sensory nerves and protecting | |
| CC | peripheral nerve cells under conditions that normally cause neuropathy. A | |
| CC | variety of neuromuscular disorders may be treated: Guillain-Barre | |
| CC | syndrome, GBS; peripheral neuropathy; diabetic neuropathy; alcohol- | |
| CC | induced neuropathy; chronic inflammatory demyelinating polyneuropathy, | |
| CC | CIPD; infection-induced neuropathy, including HIV infection; inflammation | |
| CC | -induced neuropathy; hereditary neuropathy e.g. Charcot-Marie-Tooth | |
| CC | disease (CMT), Familial Amyloidotic neuropathy, Refsum's disease, | |
| CC | Abetalipoproteinemia, Tangier disease, Krabbe's disease, Metachromatic | |
| CC | leukodystrophy, Fabry's disease, Dejerine-Sottas syndrome, Hereditary | |
| CC | sensory neuropathy Type II (HSN II) and Amyotrophic lateral sclerosis | |
| CC | (ALS); acute neuropathy e.g. Miller-Fisher syndrome; neuropathy caused by | |
| CC | vasculitis; neuropathy associated with tumours e.g. lung cancer, multiple | |
| CC | myeloma, B-cell lymphoma, Waldenstrom's Macroglobulaemia, Chronic | |
| CC | Lymphocytic Leukaemia; neuropathy associated with: amyloidosis, | |
| CC | nutritional imbalance, kidney disease, trauma; and hypothyroid | |
| CC | neuropathy. The coding sequence may be used in gene therapy of the above | |
| CC | disorders | |
| XX | | |
| SQ | Sequence 437 AA; | |
| | Query Match 83.6%; Score 2065; DB 3; Length 437; | |
| | Best Local Similarity 87.2%; Pred. No. 1.6e-180; | |
| | Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3; | |
| QY | 1 MLLARCLLLVSVSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLGASG 60 | |
| Db | 2 LLLARCFVLVILASSLLVCPGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLGASG 61 | |
| QY | 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 120 | |
| Db | 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 121 | |

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYYESKAH 180
:|||||
Db 122 RLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
:|||||
Db 182 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
:|||||
Db 242 FLDRDEGAKKVYVIETLEPRERLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVRVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
:|||||
Db 287 PSALFASRVPRGQVRVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFAFPRFLAHALLAALAPARTDRGGSDGGDRGGGGRVALTAPGA 420
:|||||
Db 347 ASCYAVIEHSHWAHRAFAFPRFLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
:|||||
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMHPGLGMVAVKSS 437

RESULT 41
AAAY70679
ID AAY70679 standard; protein; 437 AA.

XX AC AAY70679;
XX DT 18-JUL-2000 (first entry)
XX DE Mouse Sonic hedgehog (Shh) protein.
XX KW Sonic hedgehog; Shh; mouse; growth modulator; therapeutic agent; lung;
KW hedgehog; hh; patched; ptc; fibroblast growth factor; fgf-10;
KW antiproliferative; anticancer; vulnery; antirheumatic; hypotensive;
KW anti-inflammatory; antiasthmatic; antiarthritic; tuberculostatic; asthma;
KW antimicrobial; antiallergy; treatment; prevention; lung diseases; cancer;
KW cystic fibrosis; bronchitis; emphysema; respiratory distress syndrome;
KW tuberculosis; wound healing; lung transplantation.
XX OS Mus sp.

XX PN WO200015246-A2.
XX PD 23-MAR-2000.
XX PF 10-SEP-1999; 99WO-US020500.
XX PR 11-SEP-1998; 98US-0099952P.
XX PA (HARD) HARVARD COLLEGE.
XX PI Pepicelli C, Lewis P, McMahon AP;
XX DR WPI; 2000-271252/23.
XX DR N-PSDB; AAZ52260.
XX PT Modulation of lung tissue or cell growth rate used for treating or
PT preventing damage to lung tissue comprises ectopically contacting tissue
PT with hedgehog therapeutic, patched therapeutic or fibroblast growth
PT factor-10.
XX PS Claim 14; Page 119-121; 143pp; English.

XX CC The patent discloses a method for modulating the growth state of
CC epithelial or mesenchymal cells of the lung, by ectopically contacting
CC the tissue with a therapeutic agent, that can effectively alter the rate
CC of proliferation of cells. This agent can be selected from hedgehog (hh),
XX patched (ptc) or fibroblast growth factor (fgf)-10 therapeutics. It

CC involves a direct or indirect antagonism of patched-mediated regulation
CC of gene expression. This method is useful for the treatment or prevention
CC of lung diseases, like cancer, cystic fibrosis, bronchopneumoconiosis,
CC bronchitis, bronchospasm, sarcoidosis, silicosis, eosinophilic granuloma,
CC ankylosing spondylitis, emphysema, tuberculosis, respiratory distress
CC syndrome, allergic rhinitis, asthma, pulmonary fibrosis and primary
CC pulmonary hypertension. It is also used to control wound healing or other
CC reformation processes in the lung and augment lung transplantation. The
CC present sequence is the mouse sonic hedgehog (Shh) protein, essential for
CC development of the respiratory system. Hedgehog polypeptides can be used
CC to control the formation and/or maintenance of the lung tissue

XX SQ Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 3; Length 437;
Best Local Similarity 87.2%; Pred. No. 1.6e-180;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
:|||||
Db 2 LLLARCFVLILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISPSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 120
:|||||
Db 62 RYEGKITPSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 121
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYYESKAH 180
:|||||
Db 122 RLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
:|||||
Db 182 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
:|||||
Db 242 FLDRDEGAKKVYVIETLEPRERLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVRVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
:|||||
Db 287 PSALFASRVPRGQVRVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFAFPRFLAHALLAALAPARTDRGGSDGGDRGGGGRVALTAPGA 420
:|||||
Db 347 ASCYAVIEHSHWAHRAFAFPRFLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
:|||||
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMHPGLGMVAVKSS 437

RESULT 42

AAAY95284
ID AAY95284 standard; protein; 437 AA.

XX AC AAY95284;
XX DT 12-SEP-2000 (first entry)
XX DE Mouse Sonic hedgehog Shh protein.

XX KW Sonic hedgehog; Shh; mouse; excitotoxicity; Parkinson's disease;
KW Huntington's disease; neuronal degeneration; neuroprotective;
KW dopaminergic; GABAergic; substantia nigra; therapy.

XX OS Mus musculus.

XX PN WO200035948-A1.

XX PD 22-JUN-2000.

XX PF 03-DEC-1999; 99WO-US028721.

CC deliver polynucleotides encoding these lipid modulators
XX
SQ Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 3; Length 437;
Best Local Similarity 87.2%; Pred. No. 1.6e-180;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLLARCLLLVLVSSLLVCGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLLARCFVLILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 122 RLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 181

QY 181 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHND-----SGTPG 286

QY 301 PRALFASRVPRGQRVVVAERDGRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQRVVVAERGDRRLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEEHSWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTPGA 420
Db 347 ASCYAVIEEHSWAHRAFAFPFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHMPLGMVKSS 437

RESULT 44
AAB84672
ID AAB84672 standard; protein; 437 AA.
XX
AC AAB84672;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a mouse hedgehog (Shh) polypeptide.
XX
KW Shh gene; hedgehog gene; T lymphocyte; patched gene; infection; diabetes;
KW nutritional deficiency; graft rejection; hyperacute response;
KW cornea transplant; autoimmune disorder; multiple sclerosis; psoriasis;
KW atopic dermatitis; inflammatory disease; proliferative disease;
KW hyperproliferative disease; eczematous dermatitis; urticaria; vasculitis;
KW scleroderma.
XX
OS Mus sp.
XX
PN WO200140438-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032590.
XX
PR 30-NOV-1999; 99US-0168112P.
XX
PA (CURI-) CURIS INC.
XX
PI Crompton T;
XX
DR WPI; 2001-441484/47.

DR N-PSDB; AAH28449.
XX
PT Modulating immune function comprises administration of a hedgehog or ptc
PT agent, for treating e.g. diabetes, eczematous dermatitis, urticaria or
PT vasculitis.
XX
PS Claim 4; Page 81-82; 105pp; English.
XX

The present sequence represents a hedgehog (Shh) polypeptide. Hedgehog
gene products and signal transduction pathways involving hedgehog are
involved in the maturation of T lymphocytes. The specification describes
a method for modulating immune function, by administration of a hedgehog
or patched (ptc) polypeptide, agonists or antagonists. The method is used
to treat disorders affecting the regulation of lymphocytes, particularly
maturation and/or activation of T lymphocytes. It is used to treat
bacterial or viral infection, diabetes, nutritional deficiencies, graft
rejection or other hyperacute response such as kidney, heart, lung, bone
marrow spleen skin or cornea transplant or autoimmune disorders such as
multiple sclerosis, psoriasis or atopic dermatitis. The method is used to
treat inflammatory, proliferative and hyperproliferative diseases, as
well as cutaneous manifestations of immunological disorders such as
eczematous dermatitis, urticaria, vasculitis and scleroderma

SQ Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 4; Length 437;
Best Local Similarity 87.2%; Pred. No. 1.6e-180;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLLARCLLLVLVSSLLVCGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLLARCFVLILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 122 RLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 181

QY 181 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHND-----SGTPG 286

QY 301 PRALFASRVPRGQRVVVAERDGRRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQRVVVAERGDRRLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEEHSWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTPGA 420
Db 347 ASCYAVIEEHSWAHRAFAFPFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHMPLGMVKSS 437

RESULT 45
AAB60263
ID AAB60263 standard; protein; 437 AA.
XX
AC AAB60263;
XX
DT 30-MAR-2001 (first entry)
XX
DE Mouse Sonic hedgehog (Shh) protein, SEQ ID NO:13.
XX
KW Hedgehog protein; polymer conjugate; polyalkene glycol group;

Db 182 IHCSVKAENSVAAKSGCGFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVETREPRERILLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 242 FLDRDEGAKKVFYVETLEPRERILLTAHLLFVAPHND-----SGPTPG 286

QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVPGQRVVVAERGDRRLPAAVHVSVTLREEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEHSHWAHRAPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAHRAPFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPPLGMVKSS 437

RESULT 48

AAB85736

ID AAB85736 standard; protein; 437 AA.

XX

AC AAB85736;

XX

DT 29-OCT-2001 (first entry)

XX

DE Mouse sonic hedgehog (Shh) polypeptide.

XX

KW Hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh; Dhh;

KW desert hedgehog; cell differentiation; mouse.

XX

OS Mus sp.

XX

PN US6271363-B1.

XX

PD 07-AUG-2001.

XX

PF 20-OCT-1997; 97US-00954698.

XX

PR 30-DEC-1993; 93US-00176427.

PR 14-DEC-1994; 94US-00356060.

PR 04-MAY-1995; 95US-00435093.

PR 05-JUN-1995; 95US-00462386.

XX

PA (HARD) HARVARD COLLEGE.

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX

PI Ingham PW, McMahon AP, Tabin CJ;

XX

DR WPI; 2001-456723/49.

DR N-PSDB; AAH76110.

XX

PT Novel nucleic acid encoding a hedgehog polypeptide, used to produce the

PT polypeptide, which is used to promote proliferation, survival, and/or

PT differentiation of neuronal and mesodermal tissue.

XX

PS Claim 1; Col 127-130; 118pp; English.

XX

CC The invention relates to nucleic acids encoding hedgehog proteins

CC selected from sonic hedgehog (Shh), indian hedgehog (Ihh), desert

CC hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the

CC formation of ordered spatial arrangements of differentiated tissue in

CC vertebrates. The nucleic acid sequences are useful for producing hedgehog

CC proteins, used for promoting differentiation of, or survival of

CC differentiated, neuronal cells, and for promoting proliferation, survival

CC or differentiation of mesenchymal, endodermal or ectodermal tissue,

CC particularly chondrocytes, or testicular germ line cells. The present

CC sequence represents a mouse Shh polypeptide

XX

SQ Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 4; Length 437;

Best Local Similarity 87.2%; Pred. No. i.6e-180;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MILLARCLLLVLSLLVCSGLACGPGRGFGKRHPKLTPLAYKQFIENVAEKTLGASG 60

Db 2 LLLARCFVLILASSLLVCPGLACGPGRGFGKRHPKLTPLAYKQFIENVAEKTLGASG 61

QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQCKDKLNALATSVMNQWPGV 120

Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQCKDKLNALATSVMNQWPGV 121

QY 121 KLRVTEGWDEDEGHHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGEDWVYVESKAH 180

Db 122 KLRVTEGWDEDEGHHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGEDWVYVESKAH 181

QY 181 IHCSVKAENSVAAKSGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 182 IHCSVKAENSVAAKSGCGFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVETREPRERILLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 242 FLDRDEGAKKVFYVETLEPRERILLTAHLLFVAPHND-----SGPTPG 286

QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVPGQRVVVAERGDRRLPAAVHVSVTLREEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEHSHWAHRAPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAHRAPFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPPLGMVKSS 437

RESULT 49

AAG65746

ID AAG65746 standard; protein; 437 AA.

XX

AC AAG65746;

XX

DT 07-JAN-2002 (first entry)

XX

DE Mouse sonic hedgehog (Shh) polypeptide.

XX

KW Adipocyte; hedgehog polypeptide; desert hedgehog; indian hedgehog; Dhh;

KW Ihh; sonic hedgehog; Shh; therapeutic; cytostatic; tumor.

XX

OS Mus sp.

XX

PN WO200164238-A2.

XX

PD 07-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US006450.

XX

PR 29-FEB-2000; 2000US-0186058P.

XX

PA (CURI-) CURIS INC.

XX

PI Zehentner B, Leser-Reiff U, Burtscher H;

XX

DR WPI; 2001-607352/69.

DR N-PSDB; AAI66774.

XX

PT Method for regulating formation and/or maintenance of adipocyte tissue by

PT contacting pre-adipocyte or adipocyte cells with a hedgehog polypeptide

PT or ptc therapeutic.

XX

PS Disclosure; Page 97-99; 132pp; English.

XX

Db 347 ASCYAVIEHSHWAFAPFRLAHALLAALAPARTD-----CGGGGSIP-AAQSA 395

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Search completed: March 29, 2004, 18:32:03

Job time : 64 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 29, 2004, 18:30:54 ; Search time 23 Seconds
(without alignments)
1066.189 Million cell updates/sec

Title: US-09-883-848A-15
Perfect score: 2469
Sequence: 1 MLLLRCLLVSVLLVCS.....GMAVKSSXSRGAGGAREGA 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
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| 2 | 2467 | 99.9 | 475 | 3 | US-08-460-900C-13 |
| 3 | 2467 | 99.9 | 475 | 3 | US-08-674-509B-13 |
| 4 | 2467 | 99.9 | 475 | 3 | US-08-954-698-13 |
| 5 | 2467 | 99.9 | 475 | 4 | US-08-957-874-13 |
| 6 | 2467 | 99.9 | 475 | 4 | US-09-325-256-22 |
| 7 | 2467 | 99.9 | 475 | 4 | US-09-639-695-13 |
| 8 | 2467 | 99.9 | 475 | 4 | US-09-448-188-13 |
| 9 | 2467 | 99.9 | 475 | 4 | US-09-704-917-15 |
| 10 | 2467 | 99.9 | 475 | 4 | US-08-954-128-13 |
| 11 | 2467 | 99.9 | 475 | 4 | US-08-954-740-13 |
| 12 | 2467 | 99.9 | 475 | 4 | US-09-151-999-15 |
| 13 | 2467 | 99.9 | 475 | 4 | US-09-736-476-13 |
| 14 | 2407 | 97.5 | 462 | 1 | US-08-748-591-4 |
| 15 | 2407 | 97.5 | 462 | 1 | US-08-748-591-9 |
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| 24 | 2065 | 83.6 | 437 | 2 | US-08-356-060A-11 |
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| 122 | 1183 | 47.9 | 396 | 4 | US-09-736-476-9 | Sequence 9, Appli |
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| 124 | 1177 | 47.7 | 396 | 4 | US-09-704-917-17 | Sequence 17, Appl |
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| 126 | 1031 | 41.8 | 221 | 3 | US-08-460-900C-40 | Sequence 40, Appl |
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ALIGNMENTS

RESULT 1
US-08-356-060A-13
; Sequence 13, Application US/08356060A
; Patent No. 5844079
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-060A-13

Query Match          99.9%; Score 2467; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAYKSSXSRGAGGGAREGA 475

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APPLICANT: Marti-Gorostiza, Elisa
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,900C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-900C-13

Query Match 99.9%; Score 2467; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MLLARCLLLVLSLLVCSGLACGPGRGFKRRHPKCLTPLAYKQFIPNVAEKTIGASG 60
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US-08-674-509B-13
Sequence 13, Application US/08674509B
Patent No. 6261786
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
APPLICANT: Marigo, Valeria
TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,509B
FILING DATE: 02-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/460,900
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-674-509B-13

Query Match 99.9%; Score 2467; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MLLARCLLLVLSLLVCSGLACGPGRGFKRRHPKCLTPLAYKQFIPNVAEKTIGASG 60
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; Patent No. 6271363
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/954,698
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 04-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HNV-006.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-954-698-13

Query Match 99.9%; Score 2467; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
DB 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
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DB 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 5
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; Sequence 13, Application US/08957874
; Patent No. 6384192
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,874
FILING DATE: 20-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:

```

; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 475 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-957-874-13

Query Match          99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTLGASG 60
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTLGASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLS EEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLS EEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWTYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWTYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 6
US-09-325-256-22
; Sequence 22, Application US/09325256
; Patent No. 644793
; GENERAL INFORMATION:
; APPLICANT: PEPINSKY, R. BLAKE
; APPLICANT: BAKER, DARREN P.
; APPLICANT: WEN, DINGYI
; APPLICANT: WILLIAMS, KEVIN P.
; APPLICANT: GARGER, ELLEN A.
; APPLICANT: TAYLOR, FREDERICK R.
; APPLICANT: GALDES, ALPHONSE
; APPLICANT: PORTER, JEFFREY
; TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
; FILE REFERENCE: BIV-067.01
; CURRENT APPLICATION NUMBER: US/09/325,256
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/099,800
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/078,935
; PRIOR FILING DATE: 1998-03-20
;

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; PRIOR APPLICATION NUMBER: 60/089,685
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/067,423
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: PCT/US98/25676
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Xaa may be any amino acid
US-09-325-256-22

Query Match          99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTLGASG 60
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTLGASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLS EEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLS EEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWTYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWTYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 7
US-09-639-695-13
; Sequence 13, Application US/09639695
; Patent No. 6576237
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; McMahon, Andrew P.
; Tabin, Clifford J.
; Bumcrot, David A.
; Marti-Gorostiza, Elisa
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
;

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/639,695
FILING DATE: 16-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-639-695-13

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSVSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 1 MLLARCLLLVSVSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSITLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSITLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAPAPFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAPAPFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGGAREGA 475

RESULT 8
US-09-448-188-13
; Sequence 13, Application US/09448188
; Patent No. 6607913
; GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
McMahon, Andrew P.
Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,188
FILING DATE: 23-No. 6607913-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/435,093
FILING DATE: 04-MAY-1995
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-448-188-13

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVSVSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 1 MLLARCLLLVSVSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSITLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSITLSEEAAGAYAPLTAQGTILINRVL 360

| | | | |
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| QY | 361 | ASCYAVIEHSHWAHRAPAFPRFLAHALLAALAPARTDRGGDSGGGDRGGGRVALTAPGA | 420 |
| Dd | 361 | ASCYAVIEHSHWAHRAPAFPRFLAHALLAALAPARTDRGGDSGGGDRGGGRVALTAPGA | 420 |
| QY | 421 | ADAPGAGATAGIHWYSQLLYOIGTWTLLDSEALHPLGMVAKSXSRRGAGGGAREGA | 475 |
| Dd | 421 | ADAPGAGATAGIHWYSQLLYOIGTWTLLDSEALHPLGMVAKSXSRRGAGGGAREGA | 475 |

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RESULT 9
US-08-954-128-13
; Sequence 13, Application US/08954128
; Patent No. 6610656
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA

```

[illegible]

| | | | |
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| db | 61 | RYEGKISRNSERFXELTPNYNPDIIFKOEENTGADRLMTQRCCKDLNALAISVMNQPGV | 120 |
| QY | 121 | KL RVTEGWEDEGHHSSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH | 180 |
| db | 121 | KL RVTEGWEDEGHHSSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH | 180 |
| QY | 181 | IHCSVKAENSVAAKSGGPPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT | 240 |
| db | 181 | IHCSVKAENSVAAKSGGPPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT | 240 |
| QY | 241 | FLDRDDGAKKVFYVETREPRERLLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG | 300 |
| db | 241 | FLDRDDGAKKVFYVETREPRERLLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG | 300 |
| QY | 301 | PRALFASRVPRGQRVYVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL | 360 |
| db | 301 | PRALFASRVPRGQRVYVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL | 360 |
| QY | 361 | ASCYAVIEHSHWAHRAPFRLAHALLAALAPARTDRGGDSGGDRGGGGRRVALTPAGA | 420 |
| db | 361 | ASCYAVIEHSHWAHRAPFRLAHALLAALAPARTDRGGDSGGDRGGGGRRVALTPAGA | 420 |
| QY | 421 | ADAPGAGATAGIHWYSOLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA | 475 |
| db | 421 | ADAPGAGATAGIHWYSOLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA | 475 |

RESULT 10
 US-09-704-917-15
 ; Sequence 15, Application US/09704917
 ; Patent No. 6616926
 ; GENERAL INFORMATION:
 ; APPLICANT: Biogen, Inc.
 ; APPLICANT: Burkly, Linda
 ; APPLICANT: Wang, Li Chun
 ; TITLE OF INVENTION: METHODS OF MODULATING LIPID METABOLISM AND STORAGE
 ; FILE REFERENCE: A069PCT
 ; CURRENT APPLICATION NUMBER: US/09/704,917
 ; CURRENT FILING DATE: 2000-11-02
 ; PRIOR APPLICATION NUMBER: 60/122,640
 ; PRIOR FILING DATE: 1999-03-03
 ; PRIOR APPLICATION NUMBER: 60/124,446
 ; PRIOR FILING DATE: 1999-03-15
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 475
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
 US-09-704-917-15

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 99.9%; | Score 2467; | DB 4; | Length 475; |
| Best Local Similarity | 100.0%; | Pred. No. 1.9e-238; | | |
| Matches 475; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|-----|-----|---|-----|
| Qy | 1 | M L L A R C L L L V L V S S L L V C S G I A C G P G R G F G K R R H P K K L T P L A Y K Q F I P N V A E K T L G A S G | 60 |
| D b | 1 | M L L A R C L L L V L V S S L L V C S G I A C G P G R G F G K R R H P K K L T P L A Y K Q F I P N V A E K T L G A S G | 60 |
| Qy | 61 | R Y E G K I S R N S E R F K E L T P N T Y N P D I I F K D E N T G A D R L M T O R C K D K L N A L A I S V M N Q W P G V | 120 |
| D b | 61 | R Y E G K I S R N S E R F K E L T P N T Y N P D I I F K D E N T G A D R L M T O R C K D K L N A L A I S V M N Q W P G V | 120 |
| Qy | 121 | K L R V T E G W D E D G H H S E E S L H Y E G R A V D I T T S D R D R S K Y G M L A R L A V E A G F D W V Y Y E S K A H | 180 |
| D b | 121 | K L R V T E G W D E D G H H S E E S L H Y E G R A V D I T T S D R D R S K Y G M L A R L A V E A G F D W V Y Y E S K A H | 180 |
| Qy | 181 | I H C S V K A E N S V A A K S G G C F P G S A T V H L E Q G G T K L V K D L S P G D R V L A A D D Q G R L L Y S D F L T | 240 |
| D b | 181 | I H C S V K A E N S V A A K S G G C F P G S A T V H L E Q G G T K L V K D L S P G D R V L A A D D Q G R L L Y S D F L T | 240 |

QY 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
DB 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPCQVYVVAERDGDRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
DB 301 PRALFASRVPCQVYVVAERDGDRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
DB 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
DB 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 11
US-08-954-740-13
; Sequence 13, Application US/08954740
; Patent No. 6630148
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,740
; FILING DATE: 20-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,386
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 04-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 475 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-954-740-13

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
DB 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
DB 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
DB 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDEFLT 240
DB 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDEFLT 240
QY 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
DB 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPCQVYVVAERDGDRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
DB 301 PRALFASRVPCQVYVVAERDGDRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
DB 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
DB 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 12
US-09-151-999-15
; Sequence 15, Application US/09151999
; Patent No. 6639051
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; TITLE OF INVENTION: POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
; FILE REFERENCE: ONV-031.02
; CURRENT APPLICATION NUMBER: US/09/151,999
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/955,552
; EARLIER FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapien Shh
; FEATURE:
; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
US-09-151-999-15

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
DB 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
DB 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
DB 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSVAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRYVVAERDGDORLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRYVVAERDGDORLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 13

US-09-736-476-13
; Sequence 13, Application US/09736476
; Patent No. 6664075

GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
McMahon, Andrew P.
Tabin, Clifford J.
Bumcrot, David A.
Marti-Gorostiza, Elisa

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
Proteins and Uses Related Thereto

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/736,476
FILING DATE: 13-Dec-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-736-476-13

Query Match 99.9%; Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.9e-238;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYVESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVYVESKAH 180
QY 181 IHCSVKAENSVAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRYVVAERDGDORLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRYVVAERDGDORLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 14

US-08-748-591-4

; Sequence 4, Application US/08748591
; Patent No. 5759811

GENERAL INFORMATION:

APPLICANT: Epstein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog Gene
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06510/067001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids

```

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-748-591-4

Query Match          97.5%; Score 2407; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.9e-232;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
   |||||||
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
   |||||||

QY 61 RYEGKISRNSERFKELTPNYPNDIIFPKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFPKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
   |||||||

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
   |||||||

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
   |||||||

QY 241 FLDRDDGAKKVFYVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
   |||||||

QY 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
   |||||||

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
   |||||||

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
   |||||||

RESULT 15
US-08-748-591-9
; Sequence 9, Application US/08748591
; Patent No. 5759811
; GENERAL INFORMATION:
; APPLICANT: Epstein, Ervin
; APPLICANT: Hu, Zhilan
; APPLICANT: Bonifas, Jeanette
; TITLE OF INVENTION: Mutant Human Hedgehog Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish and Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,591
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06510/067001

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-748-591-9

Query Match          97.5%; Score 2407; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.9e-232;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
   |||||||
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
   |||||||

QY 61 RYEGKISRNSERFKELTPNYPNDIIFPKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFPKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
   |||||||

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
   |||||||

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
   |||||||

QY 241 FLDRDDGAKKVFYVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
   |||||||

QY 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSRTLSEEAAGAYAPLTAQGTILINRVL 360
   |||||||

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
   |||||||

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462
   |||||||

RESULT 16
US-08-946-329A-20
; Sequence 20, Application US/08946329A
; Patent No. 6057091
; GENERAL INFORMATION:
; APPLICANT: Beachy, Philip A.
; APPLICANT: Porter, Jeffrey A.
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,329A
; FILING DATE: 07-OCT-1997

```


APPLICANT: Beachy, Philip A.
APPLICANT: Moon, Randall T.
APPLICANT: Porter, Jeffrey A.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,743A
FILING DATE: 07-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,357
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/349,498
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-743A-20

Query Match 83.8%; Score 2068; DB 3; Length 437;
Best Local Similarity 87.4%; Pred. No. 1.6e-198;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLIVASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRDSKYGMLARLAVEAGFDWVYYESKAH 180
Db 122 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRDSKYGMLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYFVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYFVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQRVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQRVVVAERGGDRRLLPAAVHVSVTLREEEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVTEHSHWAHRAFPRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVTEHSHWAHRAFPRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAYKSS 462

Db 396 TEARGAETAGIHWSQLLYHIGTWLLDSETMPLGMAYKSS 437
RESULT 19
US-09-057-860A-6
Sequence 6, Application US/09057860A
Patent No. 6277820
GENERAL INFORMATION:
APPLICANT: Arnon Rosenthal
APPLICANT: Mary Hynes
APPLICANT: Weilan Ye
TITLE OF INVENTION: Method Of Dopaminergic And Seratonergic
TITLE OF INVENTION: Neuron Formation From Neuroprogenitor Cells
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,860A
FILING DATE: 09-Apr-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1364
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-057-860A-6

Query Match 83.8%; Score 2068; DB 3; Length 437;
Best Local Similarity 87.4%; Pred. No. 1.6e-198;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLIVASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRDSKYGMLARLAVEAGFDWVYYESKAH 180
Db 122 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRDSKYGMLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYFVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYFVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQRVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQRVVVAERGGDRRLLPAAVHVSVTLREEEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIIP-AAQSA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLMAVKSS 437

RESULT 20
US-08-349-498-20
; Sequence 20, Application US/08349498
; Patent No. 6281332
; GENERAL INFORMATION:
; APPLICANT: Beachy, Philip A.
; APPLICANT: Moon, Randall T.
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,498
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-349-498-20

Query Match 83.8%; Score 2068; DB 3; Length 437;
Best Local Similarity 87.4%; Pred. No. 1.6e-198;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGPKRRHPKLTPLAYKQFIPNVAEKTGLGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGPKRRHPKLTPLAYKQFIPNVAEKTGLGASG 61

QY 61 RYEGKISRNSERPKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERPKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYESKAH 180
Db 122 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYESKAH 181

QY 181 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVETREPRERILLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVETREPRERILLTAAHLLFVAPHND-----SGTPPG 286

QY 301 PRALFASRVPRGQRVYVVAERDGRRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQRVYVVAERDGRRLRLPAAVHVSVTLSEEAAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIIP-AAQSA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLMAVKSS 437

RESULT 21
PCT-US95-15463-20
; Sequence 20, Application PC/TUS9515463
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15463
; FILING DATE: 01-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/080W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-15463-20

Query Match 83.8%; Score 2068; DB 5; Length 437;
Best Local Similarity 87.4%; Pred. No. 1.6e-198;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGPKRRHPKLTPLAYKQFIPNVAEKTGLGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGPKRRHPKLTPLAYKQFIPNVAEKTGLGASG 61

QY 61 RYEGKISRNSERPKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERPKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYESKAH 180
Db 122 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYESKAH 181

QY 181 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVETREPRERILLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 242 FLDRDEGAKKVFYVIETLEPRERLLTLTAHLLFVAPHND-----SGTPG 286

Qy 301 PRALFASRVPGQRYVVAERDGRLLPAAVHVSVTLSSEAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVPGQRYVVAERDGRLLPAAVHVSVTLSSEAGAYAPLTAHGTILINRVL 346

Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGSDSGGDRGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

Qy 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 396 TEARGAEPAGIHWSQLLYHIGTWLLDSEALHPLGMVKSS 437

RESULT 22

PCT-US95-15923-20

; Sequence 20, Application PC/TUS9515923

; GENERAL INFORMATION:

; APPLICANT: The Johns Hopkins University School of Medicine, et al.

; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15923

; FILING DATE: 04-DEC-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/043WO1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 437 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-15923-20

Query Match 83.8%; Score 2068; DB 5; Length 437;

Best Local Similarity 87.4%; Pred. No. 1.6e-198;

Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLIARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

Db 2 LLLIARCLFLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 61

Qy 61 RYEGKISRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120

Db 62 RYEGKITRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

Qy 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGDWWYYESKAH 180

Db 122 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGDWWYYESKAH 181

Qy 181 IHCSVKAENSVAAKSGGCGFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 182 IHCSVKAENSVAAKSGGCGFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241

Qy 241 FLDRDGAKKVFYVIETREPRERLLTLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 242 FLDRDEGAKKVFYVIETLEPRERLLTLTAHLLFVAPHND-----SGTPG 286

Qy 301 PRALFASRVPGQRYVVAERDGRLLPAAVHVSVTLSSEAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVPGQRYVVAERDGRLLPAAVHVSVTLSSEAGAYAPLTAHGTILINRVL 346

Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGSDSGGDRGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

Qy 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 396 TEARGAEPAGIHWSQLLYHIGTWLLDSEALHPLGMVKSS 437

RESULT 23

US-08-176-427B-8

; Sequence 8, Application US/08176427B

; Patent No. 5789543

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Tabin, Clifford J.

; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

; TITLE OF INVENTION: Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/176,427B

; FILING DATE: 30-DEC-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: HMI-006

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 437 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-176-427B-8

Query Match 83.6%; Score 2065; DB 1; Length 437;

Best Local Similarity 87.2%; Pred. No. 3.3e-198;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLIARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

Db 2 LLLIARCLFLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 61

Qy 61 RYEGKISRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120

Db 62 RYEGKITRNSERFKELTPNYPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

Qy 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGDWWYYESKAH 180

Db 122 RLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQVVVVAERGGDRRLLPAAVHVSVTLSREEEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTDRGGDSGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLGMVAVKSS 437

RESULT 24
US-08-356-060A-11
; Sequence 11, Application US/08356060A
; Patent No. 5844079
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,060A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI-006CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-356-060A-11
Query Match 83.6%; Score 2065; DB 2; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 60

Db 2 LLLARCLFLVILASSLLVCPGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 61
QY 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKDKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKDKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 122 RLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAKSGCGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQVVVVAERGGDRRLLPAAVHVSVTLSREEEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTDRGGDSGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFPAPRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLGMVAVKSS 437

RESULT 25
US-08-460-900C-11
; Sequence 11, Application US/08460900C
; Patent No. 6165747
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Bumcrot, David A.
; APPLICANT: Marti-Gorostiza, Elisa
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,900C
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI-006.05

Db 182 IHCSVKAENSVAAKSGCGCPGSGATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVVIETREPRERILLTAAHLLFVAPHNDSATGEPEASSGSGPFGGALG 300
Db 242 FLDRDEGAKKVYVVIETLEPRERILLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQVVVVAERGGDRLLPAAVHSVTLREBEAGAYAPLTAHGTLINRVL 346
QY 361 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHPLGMVAVKSS 437

RESULT 29
US-09-325-256-20
; Sequence 20, Application US/09325256
; Patent No. 6444793
; GENERAL INFORMATION:
; APPLICANT: PEPINSKY, R. BLAKE
; APPLICANT: BAKER, DARREN P.
; APPLICANT: WEN, DINGYI
; APPLICANT: WILLIAMS, KEVIN P.
; APPLICANT: GARGER, ELLEN A.
; APPLICANT: TAYLOR, FREDERICK R.
; APPLICANT: GALDES, ALPHONSE
; APPLICANT: PORTER, JEFFREY
; TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
; FILE REFERENCE: BIV-067.01
; CURRENT FILING DATE: 1999-06-03
; PRIOR FILING DATE: 1998-09-10
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1997-12-03
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-325-256-20

Query Match 83.6%; Score 2065; DB 4; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLVSVLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCLLVSVLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEGHSEESLHYEGRVADITTSRDRSKYGMRLARLAVEAGFDVWVYESKAH 180
Db 122 RLRVTEGWDEGHSEESLHYEGRVADITTSRDRSKYGMRLARLAVEAGFDVWVYESKAH 181
QY 181 IHCSVKAENSVAAKSGCGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 182 IHCSVKAENSVAAKSGCGCPGSGATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVVIETREPRERILLTAAHLLFVAPHNDSATGEPEASSGSGPFGGALG 300
Db 242 FLDRDEGAKKVYVVIETLEPRERILLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQVVVVAERGGDRLLPAAVHSVTLREBEAGAYAPLTAHGTLINRVL 346
QY 361 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETHPLGMVAVKSS 437
RESULT 30
US-09-639-695-11
; Sequence 11, Application US/09639695
; Patent No. 6576237
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Bumcrot, David A.
; APPLICANT: Marti-Gorostiza, Elisa
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/639,695
; FILING DATE: 16-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-639-695-11

Query Match 83.6%; Score 2065; DB 4; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICANT: de Sauvage, Frederic
APPLICANT: Carpenter, David A.
TITLE OF INVENTION: Patched-2
FILE REFERENCE: P1405R1
CURRENT APPLICATION NUMBER: US/09/293,505
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 60/081,884
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 14
LENGTH: 437
TYPE: PRT
ORGANISM: Mus musculus
US-09-293-505-14
Query Match 83.6%; Score 2065; DB 4; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
1 MLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
2 LLLARCLFLVILASSLLVCPGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 61
61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 120
62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 121
121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYESKAH 180
122 RLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYESKAH 181
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-736-476-11

Query Match 83.6%; Score 2065; DB 4; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
Db 2 LLLARCLFLVILASSLLVCPGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 61
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYESKAH 180
Db 122 RLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGTCLVKDLSGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGTCLVKDLSGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVYVVAERDGRRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQVYVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMPLGMVAVKSS 437
RESULT 37

US-09-293-505-14
Sequence 14, Application US/09293505
Patent No. 6348575
GENERAL INFORMATION:
APPLICANT: de Sauvage, Frederic
APPLICANT: Carpenter, David A.
TITLE OF INVENTION: Patched-2
FILE REFERENCE: P1405R1
CURRENT APPLICATION NUMBER: US/09/293,505
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 60/081,884
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 14
LENGTH: 437
TYPE: PRT
ORGANISM: Mus musculus
US-09-293-505-14
Query Match 83.5%; Score 2062; DB 4; Length 437;
Best Local Similarity 87.0%; Pred. No. 6.5e-198;
Matches 402; Conservative 10; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
Db 2 LLLARCLFLVILASSLLVCPGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTIGASG 61
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTORCKDKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYESKAH 180
Db 122 RLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGTCLVKDLSGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGTCLVKDLSGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPRGQVYVVAERDGRRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQVYVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMPLGMVAVKAS 437
RESULT 38

US-08-757-230A-2
Sequence 2, Application US/08757230A
Patent No. 6235885
GENERAL INFORMATION:
APPLICANT: Thomas M. Jessell, et al.
TITLE OF INVENTION: RAT HEDGEHOG PROTEIN-1 (VHH-1)
FILE REFERENCE: 0575/45375-1/JPW/SHS/MVM
CURRENT APPLICATION NUMBER: US/08/757,230A
CURRENT FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 437
TYPE: PRT
ORGANISM: RAT
US-08-757-230A-2

Query Match 83.4%; Score 2060; DB 3; Length 437;
Best Local Similarity 87.5%; Pred. No. 1e-197;
Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 LLLARCFVALASSLLVCPGLACGPGRGFKRQHPKLTPLAYKQFIPNVAEKTILGASG 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAR 181
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 IHCSVKAENSVAAKSGCGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 IHCSVKAENSVAAKSDGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 242 FLDRDEGAKKVFYVETREPRERLLLTAHLLFVAPHND-----SGPTPG 286
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 PRALFASRVPGQRYVVAERDGRRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 287 PSPLFASRVPGQRYVVAERGDRRLPAAVHVSVTLREEAAGAYAPLTAQGTILINRVL 346
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAP-G 419
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 347 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTD-----GGGG--SIPAPQS 394
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 420 AADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 395 VAEARGAGPPAGIHWSQLLYHIGTWLLDSETLHPLGMVAVKSS 437
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 39
US-08-757-230A-9
; Sequence 9, Application US/08757230A
; Patent No. 6235885
; GENERAL INFORMATION:
; APPLICANT: Thomas M. Jessell, et al.
; TITLE OF INVENTION: RAT HEDGEHOG PROTEIN-1 (VHH-1)
; FILE REFERENCE: 0575/45375-1/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/08/757,230A
; CURRENT FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Rat
US-08-757-230A-9

Query Match 83.4%; Score 2060; DB 3; Length 437;
Best Local Similarity 87.5%; Pred. No. 1e-197;
Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 LLLARCFVALASSLLVCPGLACGPGRGFKRQHPKLTPLAYKQFIPNVAEKTILGASG 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAR 181
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 IHCSVKAENSVAAKSGCGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 182 IHCSVKAENSVAAKSDGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 242 FLDRDEGAKKVFYVETREPRERLLLTAHLLFVAPHND-----SGPTPG 286
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 PRALFASRVPGQRYVVAERDGRRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 287 PSPLFASRVPGQRYVVAERGDRRLPAAVHVSVTLREEAAGAYAPLTAQGTILINRVL 346
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAP-G 419
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 347 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTD-----GGGG--SIPAPQS 394
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 420 AADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 395 VAEARGAGPPAGIHWSQLLYHIGTWLLDSETLHPLGMVAVKSS 437
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Query Match 83.4%; Score 2060; DB 4; Length 437;
Best Local Similarity 87.5%; Pred. No. 1e-197;
Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 LLLARCFVALASSLLVCPGLACGPGRGFKRQHPKLTPLAYKQFIPNVAEKTILGASG 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 122 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAR 181
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 IHCSVKAENSVAAKSGCGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 182 IHCSVKAENSVAAKSDGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 242 FLDRDEGAKKVFYVETREPRERLLLTAHLLFVAPHND-----SGPTPG 286
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 PRALFASRVPGQRYVVAERDGRRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 287 PSPLFASRVPGQRYVVAERGDRRLPAAVHVSVTLREEAAGAYAPLTAQGTILINRVL 346
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAP-G 419
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 347 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTD-----GGGG--SIPAPQS 394
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

| | | | | | | |
|----|-----|-----------|-----------------|-----------------|----------------------------|-----|
| QY | 301 | PRALFASRV | PGORVVVVAERDGD | RRLLPAAVHVS | VTLSEEAAGAYAPLTAQTILINRVL | 360 |
| | | | | | | |
| Dø | 287 | PSPLFASRV | PGORVVVVAERGDR | RLLPFAAVHVS | VTLSEEAAGAYAPLTADGTILINRVL | 346 |
| | | | | | | |
| QY | 361 | ASCYAVIEE | HNAHRAFAFR | LAHALLAALAPARTD | RGGDSGCGDRGGGGRRVALTAP-G | 419 |
| | | | | | | |
| Dø | 347 | ASCYAVIEE | HNAHRAFAFR | LAHALLAALAPARTD | - - - - - GGGGG--SIPAQOS | 394 |
| | | | | | | |
| QY | 420 | AADAPGAGA | TAGTIHWYSQLLYQI | GTWLLDSEALHPLGM | AVKSS | 462 |
| | | : | | | | |
| Dø | 395 | VAEARGAGP | PAGTIHWYSQLLYH | IGTWLLDSETLHPLG | MVKSS | 437 |
| | | | | | | |

RESULT 42

```

US-08-176-427B-2
; Sequence 2, Application US/08176427B
; Patent No. 5789543
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,427B
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-176-427B-2

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| | Query Match | 73.2%; | Score 1807; | DB 1; | Length 425; |
|----|---------------------------|---|---------------------|--------|-------------|
| | Best Local Similarity | 77.8%; | Pred. No. 2.2e-172; | | |
| | Matches 361; Conservative | 22; | Mismatches 37; | Indels | Gaps 6; |
| Qy | 1 | MLLLARCLLLVLVSSLLVCGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG | 60 | | |
| Dd | 4 | MLLLTRILLVGFIGALLVSSGLTCGPRGIGKRRHPKLTPLAYKQFIPNVAEKTLGASG | 63 | | |
| Qy | 61 | RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKOKLNALAISVMNQWPGV | 120 | | |
| Dd | 64 | RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKOKLNALAISVMNQWPGV | 123 | | |
| Qy | 121 | KLRVTGEWDGDGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYESKAH | 180 | | |
| Dd | 124 | KLRVTGEWDGDGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYESKAH | 183 | | |
| Qy | 181 | IHC SVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLS PGDRVLAADDQQGRLLYSDFLT | 240 | | |

```

Qy 420 AADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
   :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 395 VAEARGAGPPAGIHWYSQLLYHIGTWLLDSETLHPLGMVAVKSS 437

RESULT 41
PCT-US95-02315-2
; Sequence 2, Application PC/TUS9502315
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M.
; APPLICANT: Dodd, Jane
; APPLICANT: Roelink, Thomas
; APPLICANT: Edlund, Thomas
; TITLE OF INVENTION: DNA ENCODING A VERTEBRATE HOMOLOG OF
; TITLE OF INVENTION: HEDGEHOG, VHH-1, EXPRESSED BY THE NOTOCHORD, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02315
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: John P. White
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45375-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-02315-2

```

| | Query Match | 83.4%; | Score 2060; | DB 5; | Length 437; |
|----|-----------------------|---|-------------------|------------|-------------|
| | Best Local Similarity | 87.5%; | Pred. No. 1e-197; | | |
| | Matches 405; | Conservative 8; | Mismatches 22; | Indels 28; | Gaps 4; |
| Qy | 1 | MLLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTLGASG | 60 | | |
| Db | 2 | LLLLARCFVLVALASSLLVCPGLACGPGRGFGKQHPKKLTPLAYKQFIPNVAEKTLGASG | 61 | | |
| Qy | 61 | RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQWPGV | 120 | | |
| Db | 62 | RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQWPGV | 121 | | |
| Qy | 121 | KLRVTEGWDEDDGHHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH | 180 | | |
| Db | 122 | KLRVTEGWDEDDGHHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAR | 181 | | |
| Qy | 181 | IHCsvKAENsvAAKSGGCFPGSAtVHLEQGgTKLVKdLSPGDRVLAADDQGRLLLYSDfLT | 240 | | |
| Db | 182 | IHCsvKAENsvAAKSGDGFPGSAtVHLEQGgTKLVKdLSPGDRVLAADDQGRLLLYSDfLT | 241 | | |
| Qy | 241 | FLDRDDGAKKVFYVIETREPRERLLLTAaHLLfVAPHNdSATCEPEASSGSGPPSGGALG | 300 | | |
| Db | 242 | FLDRDEGAKKVFYVIETREPRERLLLTAaHLLfVAPHNd-----SGTPPG | 286 | | |

Db 184 IHCSVKAENSVAKSGCGCPGSGATVHLEHGCTKLVDLSPGDRVLAADADGRLLYSDFLT 243

QY 241 FLDRDDGAKKVFYVETREPRERLLTAAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298

Db 244 FLDRMDSSRKLFFYVETRQPRARLLTAAHLLFVAPQHNQSEATG-----STSG----- 292

QY 299 LGPRALFASRVPGORVVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINR 358

Db 293 ---QALFASNVKPGORVVVLGE--GGQQLLPASVHVSLSREASGAYAPLTAQGTILINR 347

QY 359 VLASCYAVIEHSHWAHFAFAPFRLAHALLAALAPARTDRGGDSGGGGRGGRVALTAP 418

Db 348 VLASCYAVIEHSHWAHFAFAPFRLAQGLLAL-----CP 381

QY 419 GAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 382 DGAIPTAATTTTGIHWYSRLLYRIGSWVLDGDALHPLGMVAPAS 425

RESULT 43

US-08-356-060A-8

; Sequence 8, Application US/08356060A

; Patent No. 5844079

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Tabin, Clifford J.

; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

; TITLE OF INVENTION: Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,060A

; FILING DATE: 14-DEC-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/176,427

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: HMI-006CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 425 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-356-060A-8

Query Match 73.2%; Score 1807; DB 2; Length 425;

Best Local Similarity 77.8%; Pred. No. 2.2e-172;

Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

QY 1 MLLARCLLVVSSLLVCSGLACPGRGFGKRRHPKKLTPLAYKQFIPNVAEKTIGASG 60

Db 4 MLLLTRILLVGFICALLVSSGLTCGPRGIGKRRHPKKLTPLAYKQFIPNVAEKTIGASG 63

QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 120

Db 64 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 123

QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

Db 124 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 183

QY 181 IHCSVKAENSVAKSGCGCPGSGATVHLEHGCTKLVDLSPGDRVLAADADGRLLYSDFLT 240

Db 184 IHCSVKAENSVAKSGCGCPGSGATVHLEHGCTKLVDLSPGDRVLAADADGRLLYSDFLT 243

QY 241 FLDRDDGAKKVFYVETREPRERLLTAAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298

Db 244 FLDRMDSSRKLFFYVETRQPRARLLTAAHLLFVAPQHNQSEATG-----STSG----- 292

QY 299 LGPRALFASRVPGORVVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINR 358

Db 293 ---QALFASNVKPGORVVVLGE--GGQQLLPASVHVSLSREASGAYAPLTAQGTILINR 347

QY 359 VLASCYAVIEHSHWAHFAFAPFRLAHALLAALAPARTDRGGDSGGGGRGGRVALTAP 418

Db 348 VLASCYAVIEHSHWAHFAFAPFRLAQGLLAL-----CP 381

QY 419 GAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSS 462

Db 382 DGAIPTAATTTTGIHWYSRLLYRIGSWVLDGDALHPLGMVAPAS 425

RESULT 44

US-08-460-900C-8

; Sequence 8, Application US/08460900C

; Patent No. 6165747

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Tabin, Clifford J.

; APPLICANT: Bumcrot, David A.

; APPLICANT: Marti-Gorostiza, Elisa

; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

; TITLE OF INVENTION: Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 62

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,900C

; FILING DATE: 5-JUNE-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/435,093

; FILING DATE: 4-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/356,060

; FILING DATE: 14-DEC-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/176,427

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: HMV-006.05

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 832-1000

; TELEFAX: (617) 832-7000

; INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-900C-8

Query Match 73.2%; Score 1807; DB 3; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 4 MLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTILGASG 63

QY 61 RYEGKISRNSERFKELTPNPNPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 64 RYEGKITRNSERFKELTPNPNPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123

QY 121 KLRVTEGWEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 124 KLRVTEGWEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 183

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADQGRLLYSDFLT 240
Db 184 IHCSVKAENSVAAKSGGCGFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYSDFLT 243

QY 241 FLDRDDGAKKVYFVIETREPRERILLTAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298
Db 244 FLDRMDSRKLFYVIETROPRLRLTAHLLFVAPQHNSQSEATG-----STSG----- 292

QY 299 LGPRALFASRVPRGQRYVYVAERDGRRLLPAAVHVSILSEEAAGAYAPLTAQGTILINR 358
Db 293 ---QALFASNVPKQRYVYVLGE--GQQLLPASVHVSLSREASGAYAPLTAQGTILINR 347

QY 359 VLASCYAVIEHSHWAHRAFAFPRLAHALLAALAPARTDRGDSGGDRGGGRVALTAP 418
Db 348 VLASCYAVIEHSHWAHRAFAFPRLAQGLLAAL-----CP 381

QY 419 GAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 382 DGAIPTAATTTGIIHWYSRLLYRIGSVWLDGDALHPLGMVAPAS 425

RESULT 45
US-08-674-509B-8
; Sequence 8, Application US/08674509B
; Patent No. 6261786
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Marigo, Valeria
; TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,509B
; FILING DATE: 02-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/460,900
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-674-509B-8

Query Match 73.2%; Score 1807; DB 3; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 4 MLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTILGASG 63

QY 61 RYEGKISRNSERFKELTPNPNPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 64 RYEGKITRNSERFKELTPNPNPDIIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123

QY 121 KLRVTEGWEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 124 KLRVTEGWEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 183

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADQGRLLYSDFLT 240
Db 184 IHCSVKAENSVAAKSGGCGFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYSDFLT 243

QY 241 FLDRDDGAKKVYFVIETREPRERILLTAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298
Db 244 FLDRMDSRKLFYVIETROPRLRLTAHLLFVAPQHNSQSEATG-----STSG----- 292

QY 299 LGPRALFASRVPRGQRYVYVAERDGRRLLPAAVHVSILSEEAAGAYAPLTAQGTILINR 358
Db 293 ---QALFASNVPKQRYVYVLGE--GQQLLPASVHVSLSREASGAYAPLTAQGTILINR 347

QY 359 VLASCYAVIEHSHWAHRAFAFPRLAHALLAALAPARTDRGDSGGDRGGGRVALTAP 418
Db 348 VLASCYAVIEHSHWAHRAFAFPRLAQGLLAAL-----CP 381

QY 419 GAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 382 DGAIPTAATTTGIIHWYSRLLYRIGSVWLDGDALHPLGMVAPAS 425

RESULT 46
US-08-954-698-8
; Sequence 8, Application US/08954698
; Patent No. 6271363
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-OCT-1997
PRIORITY APPLICATION DATA:
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
FILING DATE: 04-MAY-1995
PRIORITY APPLICATION DATA:
FILING DATE: 14-DEC-1994
PRIORITY APPLICATION DATA:
FILING DATE: 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-954-698-8

Query Match 73.2%; Score 1807; DB 3; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTGASG 60
Db 4 MLLTRILLVGFICALLVSSGLTCGPGRGFKRRHPKLTPLAYKQFIPNVAEKTGASG 63
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 64 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 124 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 183
QY 181 IHCSVKAENSVAKSGCGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 184 IHCSVKAENSVAKSGCGCPGSGATVHLEHGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 243
QY 241 FLDRDDGAKKVFYVIETREPRELLLTAAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298
Db 244 FLDRDSSRKLFYVIETROPRAELLLTAAHLLFVAPQHNQSEATG-----STSG----- 292
QY 299 LGPRALFASRVPRGQRYVVAERDQDRRLPAAVHSVTLSSEAAAGAYAPLTAQFTILINR 358
Db 293 ---QALFASNVKPGQRYVVLGE--GGQQLLPASVHSVLSREASGAYAPLTAQFTILINR 347
QY 359 VLASCYAVIEHSHWAHRAFAFPLAHALLAALAPARTDRGDSGGDRGGGGRVALTAP 418
Db 348 VLASCYAVIEHSHWAHRAFAFPLAHALLAALAPARTDRGDSGGDRGGGGRVALTAP 418
QY 419 GAADAPGACATAGIHWYSQLLYQICTWLLDSEALHPLGMAYKSS 462
Db 382 DGAIPTAATTITGIHWYSRLLYRIGSWVLDGDALHPLGMVAPAS 425

RESULT 47
US-08-957-874-8

Sequence 8, Application US/08957874
Patent No. 6384192
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,874
FILING DATE: 20-OCT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 5-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-957-874-8

Query Match 73.2%; Score 1807; DB 4; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTGASG 60
Db 4 MLLTRILLVGFICALLVSSGLTCGPGRGFKRRHPKLTPLAYKQFIPNVAEKTGASG 63
QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 64 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 124 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 183
QY 181 IHCSVKAENSVAKSGCGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 184 IHCSVKAENSVAKSGCGCPGSGATVHLEHGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 243
QY 241 FLDRDDGAKKVFYVIETREPRELLLTAAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298

Db 244 FLDRMDSSRKLFFVIETROPRARLLLTAAHLLFVAPQHNQSEATG-----STSG----- 292

QY 299 LGPRALPASRVPRGQORVVYVAERDGDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINR 358

Db 293 ---QALFASNKPGQORVVYVIGE--GGQQLLPASVHSVSLREEASGAYAPLTAQGTILINR 347

QY 359 VLASCYAVIEEHSWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAP 418

Db 348 VLASCYAVIEEHSWAHRAFAFPFRLAQLLAAL-----CP 381

QY 419 GAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462

Db 382 DGAIPATAATTTGIIHWYSRLLYRIGSVWLDGDALHPLGMVAVPAS 425

RESULT 48

US-09-325-256-17

; Sequence 17, Application US/09325256

; Patent No. 6444793

; GENERAL INFORMATION:

; APPLICANT: PEPINSKY, R. BLAKE

; APPLICANT: BAKER, DARREN P.

; APPLICANT: WEN, DINGYI

; APPLICANT: WILLIAMS, KEVIN P.

; APPLICANT: GARGER, ELLEN A.

; APPLICANT: TAYLOR, FREDERICK R.

; APPLICANT: GALDES, ALPHONSE

; APPLICANT: PORTER, JEFFREY

; TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND

; FILE REFERENCE: BIV-067.01

; CURRENT APPLICATION NUMBER: US/09/325,256

; PRIOR FILING DATE: 1999-06-03

; PRIOR APPLICATION NUMBER: 60/099,800

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/078,935

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/089,685

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/067,423

; PRIOR FILING DATE: 1997-12-03

; PRIOR APPLICATION NUMBER: PCT/US98/25676

; PRIOR FILING DATE: 1998-12-03

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Gallus sp.

US-09-325-256-17

Query Match 73.2%; Score 1807; DB 4; Length 425;

Best Local Similarity 77.8%; Pred. No. 2.2e-172;

Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLLTPLAYKQFIPNVAEKTLGASG 60

Db 4 MLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLLTPLAYKQFIPNVAEKTLGASG 63

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTORCKDKLNALAISVMNQPGV 120

Db 64 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTORCKDKLNALAISVMNQPGV 123

QY 121 KLRVTEGWDEDDHSESLHYEGRVADITTSDDRSKYGMLARLAVERAGFDWVYYESKAH 180

Db 124 KLRVTEGWDEDDHSESLHYEGRVADITTSDDRSKYGMLARLAVERAGFDWVYYESKAH 183

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 184 IHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADAGRLLYSDFLT 243

QY 241 FLDRDDGAKKVFVIETREPRERLLLTAAHLLFVAP-HNDS-ATGEPEASSSGSGPPSGGA 298

Db 244 FLDRMDSSRKLFFVIETROPRARLLLTAAHLLFVAPQHNQSEATG-----STSG----- 292

QY 299 LGPRALPASRVPRGQORVVYVAERDGDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINR 358

Db 293 ---QALFASNKPGQORVVYVIGE--GGQQLLPASVHSVSLREEASGAYAPLTAQGTILINR 347

QY 359 VLASCYAVIEEHSWAHRAFAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAP 418

Db 348 VLASCYAVIEEHSWAHRAFAFPFRLAQLLAAL-----CP 381

QY 419 GAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462

Db 382 DGAIPATAATTTGIIHWYSRLLYRIGSVWLDGDALHPLGMVAVPAS 425

RESULT 49

US-09-639-695-8

; Sequence 8, Application US/09639695

; Patent No. 6576237

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Tabin, Clifford J.

; APPLICANT: Bumcrot, David A.

; APPLICANT: Marti-Gorostiza, Elisa

; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

; Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 62

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/639,695

; FILING DATE: 16-Aug-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/435,093

; FILING DATE: 4-MAY-1995

; APPLICATION NUMBER: US 08/356,060

; FILING DATE: 14-DEC-1994

; APPLICATION NUMBER: US 08/176,427

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: HMV-006.05

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 832-1000

; TELEFAX: (617) 832-7000

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 425 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-639-695-8

Query Match 73.2%; Score 1807; DB 4; Length 425;

Best Local Similarity 77.8%; Pred. No. 2.2e-172;

Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLLTPLAYKQFIPNVAEKTLGASG 60

Db 4 MLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLLTPLAYKQFIPNVAEKTLGASG 63

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OM protein - protein search, using sw model

Run on: March 29, 2004, 18:32:09 ; Search time 46 Seconds
(without alignments)
2701.943 Million cell updates/sec

Title: US-09-883-848A-15
Perfect score: 2469
Sequence: 1 MLLLRACULLVLVSSLLVCS.....GMAVKSXSRGAGGAREGA 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 2467 | 99.9 | 475 | 8 | US-08-900-220C-15 |
| 2 | 2467 | 99.9 | 475 | 8 | US-08-954-771-13 |
| 3 | 2467 | 99.9 | 475 | 8 | US-08-462-386D-13 |
| 4 | 2467 | 99.9 | 475 | 9 | US-09-021-660A-39 |
| 5 | 2467 | 99.9 | 475 | 9 | US-09-151-999-15 |
| 6 | 2467 | 99.9 | 475 | 10 | US-09-883-848A-15 |
| 7 | 2467 | 99.9 | 475 | 10 | US-09-187-387-15 |
| 8 | 2467 | 99.9 | 475 | 10 | US-09-827-110-15 |
| 9 | 2467 | 99.9 | 475 | 10 | US-09-845-025C-15 |
| 10 | 2467 | 99.9 | 475 | 10 | US-09-451-939-15 |
| 11 | 2467 | 99.9 | 475 | 10 | US-09-238-243-15 |
| 12 | 2467 | 99.9 | 475 | 10 | US-09-736-476-13 |
| 13 | 2467 | 99.9 | 475 | 12 | US-10-244-095A-15 |
| 14 | 2407 | 97.5 | 462 | 10 | US-09-733-634-14 |
| 15 | 2407 | 97.5 | 462 | 15 | US-10-294-036-15 |

| | | | | | | |
|-----|--------|------|-----|----|-------------------|-------------------|
| 89 | 1271 | 51.5 | 411 | 10 | US-09-883-848A-16 | Sequence 16, Appl |
| 90 | 1271 | 51.5 | 411 | 10 | US-09-187-387-16 | Sequence 16, Appl |
| 91 | 1271 | 51.5 | 411 | 10 | US-09-827-110-16 | Sequence 16, Appl |
| 92 | 1271 | 51.5 | 411 | 10 | US-09-845-025C-16 | Sequence 16, Appl |
| 93 | 1271 | 51.5 | 411 | 10 | US-09-451-939-16 | Sequence 16, Appl |
| 94 | 1271 | 51.5 | 411 | 10 | US-09-238-243-16 | Sequence 16, Appl |
| 95 | 1271 | 51.5 | 411 | 12 | US-09-244-095A-16 | Sequence 16, Appl |
| 96 | 1266 | 51.3 | 411 | 10 | US-09-733-634-28 | Sequence 28, Appl |
| 97 | 1266 | 51.3 | 411 | 15 | US-10-294-036-16 | Sequence 16, Appl |
| 98 | 1262 | 51.1 | 449 | 9 | US-09-990-046-29 | Sequence 29, Appl |
| 99 | 1262 | 51.1 | 449 | 10 | US-09-733-634-30 | Sequence 30, Appl |
| 100 | 1248 | 50.5 | 411 | 15 | US-10-294-036-12 | Sequence 12, Appl |
| 101 | 1234 | 50.0 | 411 | 8 | US-08-900-220C-12 | Sequence 12, Appl |
| 102 | 1234 | 50.0 | 411 | 8 | US-08-954-771-10 | Sequence 10, Appl |
| 103 | 1234 | 50.0 | 411 | 8 | US-08-462-386D-10 | Sequence 10, Appl |
| 104 | 1234 | 50.0 | 411 | 9 | US-09-151-999-12 | Sequence 12, Appl |
| 105 | 1234 | 50.0 | 411 | 10 | US-09-883-848A-12 | Sequence 12, Appl |
| 106 | 1234 | 50.0 | 411 | 10 | US-09-187-387-12 | Sequence 12, Appl |
| 107 | 1234 | 50.0 | 411 | 10 | US-09-827-110-12 | Sequence 12, Appl |
| 108 | 1234 | 50.0 | 411 | 10 | US-09-845-025C-12 | Sequence 12, Appl |
| 109 | 1234 | 50.0 | 411 | 10 | US-09-451-939-12 | Sequence 12, Appl |
| 110 | 1234 | 50.0 | 411 | 10 | US-09-238-243-12 | Sequence 12, Appl |
| 111 | 1234 | 50.0 | 411 | 10 | US-09-736-476-10 | Sequence 10, Appl |
| 112 | 1234 | 50.0 | 411 | 12 | US-10-244-095A-12 | Sequence 12, Appl |
| 113 | 1183 | 47.9 | 396 | 8 | US-08-900-220C-11 | Sequence 11, Appl |
| 114 | 1183 | 47.9 | 396 | 8 | US-08-954-771-9 | Sequence 9, Appl |
| 115 | 1183 | 47.9 | 396 | 8 | US-08-462-386D-9 | Sequence 9, Appl |
| 116 | 1183 | 47.9 | 396 | 9 | US-09-021-660A-35 | Sequence 35, Appl |
| 117 | 1183 | 47.9 | 396 | 9 | US-09-151-999-11 | Sequence 11, Appl |
| 118 | 1183 | 47.9 | 396 | 9 | US-09-990-046-13 | Sequence 13, Appl |
| 119 | 1183 | 47.9 | 396 | 10 | US-09-733-634-22 | Sequence 22, Appl |
| 120 | 1183 | 47.9 | 396 | 10 | US-09-883-848A-11 | Sequence 11, Appl |
| 121 | 1183 | 47.9 | 396 | 10 | US-09-187-387-11 | Sequence 11, Appl |
| 122 | 1183 | 47.9 | 396 | 10 | US-09-827-110-11 | Sequence 11, Appl |
| 123 | 1183 | 47.9 | 396 | 10 | US-09-845-025C-11 | Sequence 11, Appl |
| 124 | 1183 | 47.9 | 396 | 10 | US-09-451-939-11 | Sequence 11, Appl |
| 125 | 1183 | 47.9 | 396 | 10 | US-09-238-243-11 | Sequence 11, Appl |
| 126 | 1183 | 47.9 | 396 | 10 | US-09-736-476-9 | Sequence 9, Appl |
| 127 | 1183 | 47.9 | 396 | 12 | US-10-244-095A-11 | Sequence 11, Appl |
| 128 | 1183 | 47.9 | 396 | 15 | US-10-294-036-11 | Sequence 11, Appl |
| 129 | 1177 | 47.7 | 396 | 8 | US-08-900-220C-17 | Sequence 17, Appl |
| 130 | 1177 | 47.7 | 396 | 9 | US-09-151-999-17 | Sequence 17, Appl |
| 131 | 1177 | 47.7 | 396 | 10 | US-09-883-848A-17 | Sequence 17, Appl |
| 132 | 1177 | 47.7 | 396 | 10 | US-09-187-387-17 | Sequence 17, Appl |
| 133 | 1177 | 47.7 | 396 | 10 | US-09-827-110-17 | Sequence 17, Appl |
| 134 | 1177 | 47.7 | 396 | 10 | US-09-845-025C-17 | Sequence 17, Appl |
| 135 | 1177 | 47.7 | 396 | 10 | US-09-451-939-17 | Sequence 17, Appl |
| 136 | 1177 | 47.7 | 396 | 10 | US-09-238-243-17 | Sequence 17, Appl |
| 137 | 1177 | 47.7 | 396 | 12 | US-10-244-095A-17 | Sequence 17, Appl |
| 138 | 1177 | 47.7 | 396 | 15 | US-10-294-036-17 | Sequence 17, Appl |
| 139 | 1174 | 47.5 | 396 | 14 | US-10-147-463-3 | Sequence 3, Appl |
| 140 | 1170 | 47.4 | 396 | 9 | US-09-244-466-2 | Sequence 2, Appl |
| 141 | 1163.5 | 47.1 | 374 | 14 | US-10-147-463-2 | Sequence 2, Appl |
| 142 | 1055.5 | 42.8 | 336 | 9 | US-09-021-660A-36 | Sequence 36, Appl |
| 143 | 1031 | 41.8 | 221 | 8 | US-08-900-220C-21 | Sequence 21, Appl |
| 144 | 1031 | 41.8 | 221 | 8 | US-08-954-771-40 | Sequence 40, Appl |
| 145 | 1031 | 41.8 | 221 | 8 | US-08-462-386D-40 | Sequence 40, Appl |
| 146 | 1031 | 41.8 | 221 | 9 | US-09-151-999-21 | Sequence 21, Appl |
| 147 | 1031 | 41.8 | 221 | 10 | US-09-187-387-21 | Sequence 21, Appl |
| 148 | 1031 | 41.8 | 221 | 10 | US-09-827-110-21 | Sequence 21, Appl |
| 149 | 1031 | 41.8 | 221 | 10 | US-09-845-025C-21 | Sequence 21, Appl |
| 150 | 1031 | 41.8 | 221 | 10 | US-09-451-939-21 | Sequence 21, Appl |

ALIGNMENTS

RESULT 1
US-08-900-220C-15
; Sequence 15, Application US/08900220C
; Publication No. US20020045206A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Ningning

Wang, Monica
Mahanthappa, Nagesh K.
Pang, Kevin
Jin, Ping
TITLE OF INVENTION: Method of Treating Dopaminergic and
GABA-nergic Disorders
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: ONE POST OFFICE SQUARE
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,220C
FILING DATE: 24-Jul-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: ONV-044.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-900-220C-15
Query Match 99.9%; Score 2467; DB 8; Length 475;
Best local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLLRCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTGLGSG 60
Db 1 MLLLRCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTGLGSG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIFKDEENTGADRLMTORCKDLNALAISVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYNPDIFKDEENTGADRLMTORCKDLNALAISVMNQPGV 120
QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDEFLT 240
Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDEFLT 240
QY 241 FLDRDDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVRCQRVVYVAERDGDRLRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVRCQRVVYVAERDGDRLRLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEEHSWAHRAFAFPRLAHALLAALAPARTDRGGDSGGGDRGGGRVALTPGA 420
Db 361 ASCYAVIEEHSWAHRAFAFPRLAHALLAALAPARTDRGGDSGGGDRGGGRVALTPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSSXSRCAGGGAREGA 475

Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

RESULT 2

US-08-954-771-13

; Sequence 13, Application US/08954771

; Publication No. US20030054437A1

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Tabin, Clifford J.

; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

; TITLE OF INVENTION: Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/954,771

; FILING DATE: 20-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/462,386

; FILING DATE: 05-JUN-1995

; APPLICATION NUMBER: US 08/435,093

; FILING DATE: 04-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/356,060

; FILING DATE: 14-DEC-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/176,427

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: HMV-006.11

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 475 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-954-771-13

Query Match 99.9%; Score 2467; DB 8; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.1e-207;

Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLLARCLLLVLSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

Db 1 MLLLARCLLLVLSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

Qy 61 RYEGKTSRNSERFKELTPNPNPDIFKDEENTGADRLMTQCKDKLNALAISVMNQPGV 120

Db 61 RYEGKTSRNSERFKELTPNPNPDIFKDEENTGADRLMTQCKDKLNALAISVMNQPGV 120

Qy 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

Db 121 KLRVTEGWDEDDGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

Qy 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Qy 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300

Db 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300

Qy 301 PRALFASRVPRGQRVVVAERDGRRLLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVPRGQRVVVAERDGRRLLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420

Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420

Qy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

RESULT 3

US-08-462-386D-13

; Sequence 13, Application US/08462386D

; Publication No. US20030186357A1

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Tabin, Clifford J.

; TITLE OF INVENTION: Vertebrate Tissue Pattern-Inducing

; TITLE OF INVENTION: Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,386D

; FILING DATE: 5-JUNE-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/435,093

; FILING DATE: 4-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/356,060

; FILING DATE: 14-DEC-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/176,427

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: HMI-006CP3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 475 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-462-386D-13

Query Match 99.9%; Score 2467; DB 8; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.1e-207;

Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 4

US-09-021-660A-39
; Sequence 39, Application US/09021660A
; Patent No. US20010041668A1
; GENERAL INFORMATION:
; APPLICANT: Baron, M.
; APPLICANT: Farrington, S.
; APPLICANT: Belaussoff, M.
; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: HUIP-P01-060
; CURRENT APPLICATION NUMBER: US/09/021,660A
; PRIOR FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1997-02-10
; PRIOR FILING DATE: 1997-02-10
; PRIOR FILING DATE: 1997-06-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (463)
; OTHER INFORMATION: Xaa=unknown amino acid
US-09-021-660A-39

Query Match 99.9%; Score 2467; DB 9; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120

Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 5

US-09-151-999-15
; Sequence 15, Application US/09151999
; Patent No. US20020151460A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; TITLE OF INVENTION: POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
; FILE REFERENCE: ONV-031.02
; CURRENT APPLICATION NUMBER: US/09/151,999
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/955,552
; EARLIER FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapien Shh
; FEATURE:
; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
US-09-151-999-15

Query Match 99.9%; Score 2467; DB 9; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTLCASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

RESULT 6
US-09-883-848A-15
; Sequence 15, Application US/09883848A
; Publication No. US20030022819A1
; GENERAL INFORMATION:
; APPLICANT: Ling, L.
; APPLICANT: Sanicola-Nadel, M.
; TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
; FILE REFERENCE: CIBT-P01-119
; CURRENT APPLICATION NUMBER: US/09/883,848A
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/211,919
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (463)
; OTHER INFORMATION: xaa-unknown amino acid residue
US-09-883-848A-15

Query Match 99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKCLTPLAYKQFIPNVAEKTGLGASG 60
Db 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKCLTPLAYKQFIPNVAEKTGLGASG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFFVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFFVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475
RESULT 7
US-09-187-387-15
; Sequence 15, Application US/09187387
; Publication No. US20030083242A1
; GENERAL INFORMATION:
; APPLICANT: Galdes, Alphonse
; APPLICANT: Mahanthappa, Nagesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: PERIPHERAL NEUROPATHIES
; FILE REFERENCE: ONV-052.01
; CURRENT APPLICATION NUMBER: US/09/187,387
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 475
; TYPE: PRT
; ORGANISM: human Shh
; FEATURE:
; OTHER INFORMATION: xaa at position 463 is any or unknown amino acid
US-09-187-387-15

Query Match 99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKCLTPLAYKQFIPNVAEKTGLGASG 60
Db 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFKRRHPKCLTPLAYKQFIPNVAEKTGLGASG 60
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFFVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFFVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSSGSGPPSGGALG 300
QY 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRGQVVVVAERDGRRLLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFPFRLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAGGGAREGA 475

RESULT 8
US-09-827-110-15
; Sequence 15, Application US/09827110
; Publication No. US20030104970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; TITLE OF INVENTION: POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
; FILE REFERENCE: ONV-031.02
; CURRENT APPLICATION NUMBER: US/09/827,110
; CURRENT FILING DATE: 2000-04-05

;; PRIOR APPLICATION NUMBER: 08/955,552
;; PRIOR FILING DATE: 1997-10-20
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 15
;; LENGTH: 475
;; TYPE: PRT
;; ORGANISM: Homo sapien Shh
;; FEATURE:
;; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
US-09-827-110-15

Query Match 99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVYFVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300
Db 241 FLDRDDGAKKVYFVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300

QY 301 PRALFASRVPRQORVYVVAERDGDRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRQORVYVVAERDGDRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDGGDRGGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 9
US-09-845-025C-15
; Sequence 15, Application US/09845025C
; Publication No. US20030104995A1
; GENERAL INFORMATION:
; APPLICANT: Reilly, J.
; TITLE OF INVENTION: NEUROPROTECTIVE METHODS AND COMPOSITIONS
; FILE REFERENCE: CIBT-P01-098
; CURRENT APPLICATION NUMBER: US/09/845,025C
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,765
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 15
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (463)
; OTHER INFORMATION: Xaa=unknown amino acid residue
US-09-845-025C-15

Query Match 99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVYFVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300
Db 241 FLDRDDGAKKVYFVIETREPRERLLTTAAHLLFVAPHNDSATGEPEASSSGSPSGGALG 300

QY 301 PRALFASRVPRQORVYVVAERDGDRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRQORVYVVAERDGDRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDGGDRGGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVKSXSRGAGGGAREGA 475

RESULT 10
US-09-451-939-15
; Sequence 15, Application US/09451939
; Publication No. US20030119729A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Ningning
; APPLICANT: Wang, Monica
; APPLICANT: Mahanthappa, Nagesh K.
; APPLICANT: Jin, Ping
; APPLICANT: Pang, Kevin
; TITLE OF INVENTION: Method of Treating Dopaminergic and
; TITLE OF INVENTION: GABA-nergic Disorders
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: ONE POST OFFICE SQUARE
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,939
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/900,220
; FILING DATE: 24-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: ONV-044.01


```

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 832-1000
/ TELEFAX: (617) 832-7000
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 475 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-451-939-15

Query Match      99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTIGASG 60
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTIGASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGPPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGPPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLFFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLFFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSVTLSAAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSVTLSAAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 11
US-09-238-243-15
; Sequence 15, Application US/09238243
; Publication No. US20030162698A1
; GENERAL INFORMATION:
; APPLICANT: Galdes, Alphonse
; APPLICANT: Mahanthappa, Nagesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DOPAMINERGIC
; TITLE OF INVENTION: AND GABA-NERGIC DISORDERS
; FILE REFERENCE: ONV-069.01
; CURRENT APPLICATION NUMBER: US/09/238,243
; CURRENT FILING DATE: 1999-01-27.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapien Shh
; FEATURE:
; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
/ US-09-238-243-15

Query Match      99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTIGASG 60
Db 1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTIGASG 60
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
QY 181 IHCSVKAENSVAAKSGGCGPPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGPPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLFFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVIETREPRERLLLTAAHLFFVAPHNDSATGEPEASSGSGPPSGGALG 300
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSVTLSAAAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHVSVTLSAAAAGAYAPLTAQGTILINRVL 360
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAPGA 420
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSSXSRGAGGGAREGA 475

RESULT 12
US-09-736-476-13
; Sequence 13, Application US/09736476
; Publication No. US20030190696A1
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Bumcrot, David A.
; APPLICANT: Marti-Gorostiza, Elisa
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/736,476
; FILING DATE: 13-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
```

```

; REFERENCE/DOCKET NUMBER: HMI-006CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 475 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-736-476-13

Query Match          99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRQGVVVAERDGDRELLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRQGVVVAERDGDRELLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGLMAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGLMAVKSSXSRGAGGGAREGA 475
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RESULT 13
US-10-244-095A-15
; Sequence 15, Application US/10244095A
; Publication No. US20040038876A1
; GENERAL INFORMATION:
; APPLICANT: Pepinsky, Blake R.
; APPLICANT: Taylor, Frederick
; APPLICANT: Garber, Ellen A.
; TITLE OF INVENTION: POLYMER CONJUGATES OF HEDGEHOG PROTEINS AND USES
; FILE REFERENCE: CIBT-P01-117
; CURRENT APPLICATION NUMBER: US/10/244,095A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/14741
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/149,016
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/137,011
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 475
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (463)
; OTHER INFORMATION: Xaa=unknown amino acid residue
US-10-244-095A-15

Query Match          99.9%; Score 2467; DB 12; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120

QY 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 181 IHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 241 FLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRQGVVVAERDGDRELLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVPRQGVVVAERDGDRELLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGLMAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGLMAVKSSXSRGAGGGAREGA 475
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RESULT 14
US-09-733-634-14
; Sequence 14, Application US/09733634
; Publication No. US20030013646A1
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Method to stimulate Insulin production by pancreatic b-cells
; FILE REFERENCE: 17633/1240
; CURRENT APPLICATION NUMBER: US/09/733,634
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/170,282
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-733-634-14

Query Match          97.5%; Score 2407; DB 10; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.7e-202;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVSVLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60
Db 1 MLLARCLLLVSVLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
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Db 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV 120

QY 121 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180

Db 121 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRGORVYVVAERDGRRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVPRGORVYVVAERDGRRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSS 462

Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSS 462

RESULT 15

US-10-294-036-15

; Sequence 15, Application US/10294036

; Publication No. US20030220244A1

; GENERAL INFORMATION:

; APPLICANT: Warzecha, Joerg

; TITLE OF INVENTION: HEDGEHOG SIGNALING PROMOTES THE FORMATION OF THREE DIMENSIONAL CA

; TITLE OF INVENTION: MATRICES, METHODS AND COMPOSITIONS RELATED THERETO

; FILE REFERENCE: CIBT-P01-123

; CURRENT APPLICATION NUMBER: US/10/294,036

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 60/350,594

; PRIOR FILING DATE: 2001-11-13

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 15

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-294-036-15

Query Match 97.5%; Score 2407; DB 15; Length 462;

Best Local Similarity 100.0%; Pred. No. 3.7e-202;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTLGASG 60

Db 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV 120

Db 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV 120

QY 121 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180

Db 121 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRGORVYVVAERDGRRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

Db 301 PRALFASRVPRGORVYVVAERDGRRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSS 462

Db 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSS 462

RESULT 16

US-09-021-660A-37

; Sequence 37, Application US/09021660A

; Patent No. US20010041668A1

; GENERAL INFORMATION:

; APPLICANT: Baron, M.

; APPLICANT: Farrington, S.

; APPLICANT: Belaussoff, M.

; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR

; TITLE OF INVENTION: GROWTH

; FILE REFERENCE: HUIP-P01-060

; CURRENT APPLICATION NUMBER: US/09/021,660A

; CURRENT FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: 60/037,513

; PRIOR FILING DATE: 1997-02-10

; PRIOR APPLICATION NUMBER: 60/049,763

; PRIOR FILING DATE: 1997-06-16

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 37

; LENGTH: 437

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-021-660A-37

Query Match 83.8%; Score 2068; DB 9; Length 437;

Best Local Similarity 87.4%; Pred. No. 1.7e-172;

Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTLGASG 60

Db 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKCLTPLAYKQFIPNVAEKTLGASG 60

QY 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV 120

Db 61 RYEGKISRNSERFKELTPNYNPDIIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV 120

QY 121 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180

Db 121 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYYESKAH 180

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

QY 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 241 FLDRDDGAKKVFIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

QY 301 PRALFASRVPRGORVYVVAERDGRRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVPRGORVYVVAERDGRRLLPAAVHSTLSEEAAGAYAPLTAQGTILINRVL 346

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSS 462

Db 396 TEARGAEPTAGIHWYSQLLYQIGTWLLDSEALHPLGMAYKSS 437


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; SOFTWARE: Ascii (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,220C
; FILING DATE: 24-Jul-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: ONV-044.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-900-220C-13

Query Match      83.6%; Score 2065; DB 8; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLARCLLVVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 61

QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
122 RLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 181

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGTCLKVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGTCLKVKDLSPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
242 FLDRDEGAKKVFYVETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

QY 301 PRALFASRVRPQGVVVAERDGRRLPAVHVSVTLSSEAAGAYAPLTAQTILINRVL 360
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 PSALFASRVRPQGVVVAERDGRRLPAVHVSVTLSREEAGAYAPLTAHTGILINRVL 346

QY 361 ASCYAVIEHSHWAHAFAPFRLAHALLAALAPARTDRGDSGGGGRGGRVALTPGA 420
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
347 ASCYAVIEHSHWAHAFAPFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPPLGMVKSS 437
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; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,771
; FILING DATE: 20-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,386
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 04-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-771-11

Query Match      83.6%; Score 2065; DB 8; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLARCLLVVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 60
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASG 61

QY 61 RYEGKISRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
62 RYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121

QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 180
Db :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
122 RLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAH 181

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGTCLKVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGTCLKVKDLSPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
242 FLDRDEGAKKVFYVETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

QY 301 PRALFASRVRPQGVVVAERDGRRLPAVHVSVTLSSEAAGAYAPLTAQTILINRVL 360
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 PSALFASRVRPQGVVVAERDGRRLPAVHVSVTLSREEAGAYAPLTAHTGILINRVL 346

QY 361 ASCYAVIEHSHWAHAFAPFRLAHALLAALAPARTDRGDSGGGGRGGRVALTPGA 420
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
347 ASCYAVIEHSHWAHAFAPFRLAHALLAALAPARTD-----GGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS 462
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPPLGMVKSS 437
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Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 122 RLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPGQRVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPGQRVVVAERGGDRRLPAAVHVSVTLSSEAAAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAPAFRRLAHALLAALAPARTDRGGDSGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAPAFRRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWISQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWISQLLYHIGTWLLDSETMHPPLGMVAVKSS 437

RESULT 28
US-09-845-025C-13
; Sequence 13, Application US/09845025C
; Publication No. US20030104995A1
; GENERAL INFORMATION:
; APPLICANT: Reilly, J.
; TITLE OF INVENTION: NEUROPROTECTIVE METHODS AND COMPOSITIONS
; FILE REFERENCE: CIBT-P01-098
; CURRENT APPLICATION NUMBER: US/09/845,025C
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,765
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-025C-13

Query Match 83.6%; Score 2065; DB 10; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLIVASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAH 180
Db 122 RLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPGQRVVVAERDGRRLPAAVHVSVTLSSEAAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVPGQRVVVAERGGDRRLPAAVHVSVTLSSEAAAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAPAFRRLAHALLAALAPARTDRGGDSGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAPAFRRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWISQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWISQLLYHIGTWLLDSETMHPPLGMVAVKSS 437

RESULT 29
US-09-451-939-13
; Sequence 13, Application US/09451939
; Publication No. US20030119729A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Ningning
; APPLICANT: Wang, Monica
; APPLICANT: Mahanthappa, Nagesh K.
; APPLICANT: Jin, Ping
; APPLICANT: Pang, Kevin
; TITLE OF INVENTION: Method of Treating Dopaminergic and
; TITLE OF INVENTION: GABA-nergic Disorders
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: ONE POST OFFICE SQUARE
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,939
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/900,220
; FILING DATE: 24-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: ONV-044.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-451-939-13

Query Match 83.6%; Score 2065; DB 10; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
QY 1 MLLARCLLLVSVLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLIVASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAH 180

Db 122 RLRVTEGWDEGHHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 181

QY 181 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 182 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFFVVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 242 FLDRDEGAKKVFFVVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

QY 301 PRALFASRVRPGQRVYVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVRPGQRVYVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEEHSWAHRAFPAPRLAHALLAALAPARTDRTDGGDSGGDRGGGGRVALTPGA 420

Db 347 ASCYAVIEEHSWAHRAFPAPRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462

Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMHPPLGMVAVKSS 437

RESULT 30

US-09-238-243-13

; Sequence 13, Application US/09238243

; Publication No. US20030162698A1

; GENERAL INFORMATION:

; APPLICANT: Galdes, Alphonse

; APPLICANT: Mahanthappa, Nagesh

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DOPAMINERGIC

; TITLE OF INVENTION: AND GABA-NERGIC DISORDERS

; FILE REFERENCE: ONV-069.01

; CURRENT APPLICATION NUMBER: US/09/238,243

; CURRENT FILING DATE: 1999-01-27

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 437

; TYPE: PRT

; ORGANISM: murine Shh

US-09-238-243-13

Query Match 83.6%; Score 2065; DB 10; Length 437;

Best Local Similarity 87.2%; Pred. No. 3.2e-172;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLLARCLLVVSSLLVCVSLGACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

Db 2 LLLLARCFVLIVASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 61

QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120

Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 121

QY 121 KLRVTEGWDEGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

Db 122 RLRVTEGWDEGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 181

QY 181 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240

Db 182 IHCSVKAENSVAAKSGGCGPPGSGATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241

QY 241 FLDRDDGAKKVFFVVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300

Db 242 FLDRDEGAKKVFFVVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

QY 301 PRALFASRVRPGQRVYVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360

Db 287 PSALFASRVRPGQRVYVVAERGGDRRLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346

QY 361 ASCYAVIEEHSWAHRAFPAPRLAHALLAALAPARTDRTDGGDSGGGGRVALTPGA 420

Db 347 ASCYAVIEEHSWAHRAFPAPRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395

QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462

Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMHPPLGMVAVKSS 437

RESULT 31

US-09-736-476-11

; Sequence 11, Application US/09736476

; Publication No. US20030190696A1

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; APPLICANT: McMahon, Andrew P.

; APPLICANT: Tabin, Clifford J.

; APPLICANT: Bumcrot, David A.

; APPLICANT: Marti-Gorostiza, Elisa

; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

; TITLE OF INVENTION: Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/736,476

; FILING DATE: 13-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/435,093

; FILING DATE: 4-MAY-1995

; APPLICATION NUMBER: US 08/356,060

; FILING DATE: 14-DEC-1994

; APPLICATION NUMBER: US 08/176,427

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: HMI-006CP4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 437 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-736-476-11

Query Match 83.6%; Score 2065; DB 10; Length 437;

Best Local Similarity 87.2%; Pred. No. 3.2e-172;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

QY 1 MLLLARCLLVVSSLLVCVSLGACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 60

Db 2 LLLLARCFVLIVASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTLGASG 61

QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 120

Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV 121

QY 121 KLRVTEGWDEGHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180

Db 122 RLRVTEGWDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 181
Qy 181 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
Qy 241 FLDRDDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
Qy 301 PRALFASRVVRPGQRVVVAERDGDRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVVRPGQRVVVAERGGDRRLPAAVHVSVTLREEEAGAYAPLTAHGTILINRVL 346
Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 347 PSALFASRVVRPGQRVVVAERGGDRRLPAAVHVSVTLREEEAGAYAPLTAHGTILINRVL 346
Qy 361 PRALFASRVVRPGQRVVVAERDGDRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
Qy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLGMVAVKSS 437

RESULT 32
US-10-244-095A-13
; Sequence 13, Application US/10244095A
; Publication No. US20040038876A1
; GENERAL INFORMATION:
; APPLICANT: Pepinsky, Blake R.
; APPLICANT: Taylor, Frederick
; APPLICANT: Garber, Ellen A.
; TITLE OF INVENTION: POLYMER CONJUGATES OF HEDGEHOG PROTEINS AND USES
; FILE REFERENCE: CIBT-P01-117
; CURRENT APPLICATION NUMBER: US/10/244,095A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/14741
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/149,016
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/137,011
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-244-095A-13

Query Match 83.6%; Score 2065; DB 12; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
Qy 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
Qy 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 120
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 121
Qy 121 KLRVTEGWDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 122 RLRVTEGWDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 181
Qy 181 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
Qy 241 FLDRDDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286

Qy 301 PRALFASRVVRPGQRVVVAERDGDRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVVRPGQRVVVAERGGDRRLPAAVHVSVTLREEEAGAYAPLTAHGTILINRVL 346
Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
Qy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLGMVAVKSS 437
RESULT 33
US-10-294-036-13
; Sequence 13, Application US/10294036
; Publication No. US20030220244A1
; GENERAL INFORMATION:
; APPLICANT: Warzecha, Joerg
; TITLE OF INVENTION: HEDGEHOG SIGNALING PROMOTES THE FORMATION OF THREE DIMENSIONAL C
; TITLE OF INVENTION: MATRICES, METHODS AND COMPOSITIONS RELATED THERETO
; FILE REFERENCE: CIBT-P01-123
; CURRENT APPLICATION NUMBER: US/10/294,036
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/350,594
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-294-036-13

Query Match 83.6%; Score 2065; DB 15; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
Qy 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 120
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAISVMNQWPGV 121
Qy 121 KLRVTEGWDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
Db 122 RLRVTEGWDEGHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 181
Qy 181 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGCGPFGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
Qy 241 FLDRDDGAKKVYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLLLTAAHLLFVAPHND-----SGPTPG 286
Qy 301 PRALFASRVVRPGQRVVVAERDGDRLRLPAAVHVSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVVRPGQRVVVAERGGDRRLPAAVHVSVTLREEEAGAYAPLTAHGTILINRVL 346
Qy 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
Qy 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPGLGMVAVKSS 437

RESULT 34
US-09-990-046-14

Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 122 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAR 181
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVIETREPRERLLLTAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSPLFASRVPGQRVVVAERGGDRRLLPAAVHSVTLREEAAGAYAPLTADGTILINRVL 346
QY 361 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTDRGGDGGGGRVALTAP-G 419
Db 347 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTD-----GGGG--SIPAPQS 394
QY 420 AADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 395 VAARGAGPPAGIHWSQLLYHIGTWLLDSETLHPLGMVAVKSS 437

RESULT 37
US-09-969-520A-10
; Sequence 10, Application US/09969520A
; Patent No. US20020177163A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: BEACHY, Philip A.
; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
; FILE REFERENCE: JHU1670-1
; CURRENT APPLICATION NUMBER: US/09/969,520A
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/235,153
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Altered sonic hedgehog protein
US-09-969-520A-10

Query Match 83.4%; Score 2059; DB 9; Length 437;
Best Local Similarity 87.0%; Pred. No. 1.le-171;
Matches 402; Conservative 9; Mismatches 25; Indels 26; Gaps 3;
QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 122 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVIETREPRERLLLTAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSPLFASRVPGQRVVVAERGGDRRLLPAAVHSVTLREEAAGAYAPLTADGTILINRVL 346
QY 361 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTDRGGDGGGGRVALTAPGA 420
Db 347 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTD-----GGGG--SIPAPQS 394
QY 420 AADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 395 VAARGAGPPAGIHWSQLLYHIGTWLLDSETLHPLGMVAVKSS 437

Db 242 FLDRDEGAKKVFYVIETLEPRERLLLTAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPGQRVVVAERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTDRGGDGGGGRGRVALTAPGA 420
Db 347 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTD-----GGGG--SIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMHPPLGMVAVKSS 437
RESULT 38
US-09-969-520A-11
; Sequence 11, Application US/09969520A
; Patent No. US20020177163A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: BEACHY, Philip A.
; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
; FILE REFERENCE: JHU1670-1
; CURRENT APPLICATION NUMBER: US/09/969,520A
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/235,153
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Altered sonic hedgehog protein
US-09-969-520A-11

Query Match 83.4%; Score 2059; DB 9; Length 437;
Best Local Similarity 87.0%; Pred. No. 1.le-171;
Matches 402; Conservative 9; Mismatches 25; Indels 26; Gaps 3;
QY 1 MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLARCFVLVILASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 120
Db 62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQPGV 121
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH 180
Db 122 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYEEAAAH 181
QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVFYVIETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALG 300
Db 242 FLDRDEGAKKVFYVIETLEPRERLLLTAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASRVPGQRVVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASRVPGQRVVVAERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTDRGGDGGGGRGRVALTAPGA 420
Db 347 ASCYAVIEEHSWAHRAFPAPFRLAHALLAALAPARTD-----GGGG--SIP-AAQSA 395
QY 421 ADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWSQLLYHIGTWLLDSETMHPPLGMVAVKSS 437

QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETHPLGMVAVKSS 437
RESULT 44
US-09-969-520A-7
; Sequence 7, Application US/09969520A
; Patent No. US20020177163A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: BEACHY, Philip A.
; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
; FILE REFERENCE: JHU1670-1
; CURRENT APPLICATION NUMBER: US/09/969,520A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/235,153
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Altered sonic hedgehog protein
US-09-969-520A-7
Query Match 82.5%; Score 2036; DB 9; Length 437;
Best Local Similarity 86.1%; Pred. No. 1.1e-169;
Matches 398; Conservative 10; Mismatches 28; Indels 26; Gaps 3;
QY 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLLARCFVLIVLASSLLVCPGLACGPGRGFGKRRHPKLTALAYAQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 62 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 121
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYIESKAH 180
Db 122 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYIESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKOLRPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASVRPQGVVVAERDGRRLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASVRPQGVVVAERGDRRLPAAVHVSVTLSREEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETHPLGMVAVKSS 437
RESULT 45
US-09-969-520A-5
; Sequence 5, Application US/09969520A

; Patent No. US20020177163A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: BEACHY, Philip A.
; TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
; FILE REFERENCE: JHU1670-1
; CURRENT APPLICATION NUMBER: US/09/969,520A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/235,153
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Altered sonic hedgehog protein
US-09-969-520A-5

Query Match 81.8%; Score 2019; DB 9; Length 437;
Best Local Similarity 85.9%; Pred. No. 3.4e-168;
Matches 397; Conservative 8; Mismatches 31; Indels 26; Gaps 3;
QY 1 MLLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 2 LLLLARCFVLIVLASSLLVCPGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 61
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 62 RYEGKITRNSERFAALTNPANPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 121
QY 121 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYIESKAH 180
Db 122 KLRVTEGWDEDEGHSEESLHYEGRAVDITTSDDRDRSKYGMRLARLAVEAGFDWVYIESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSVAASGGCGPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDDGAKKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSSGPPSGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLLTAAHLLFVAPHND-----SGPTPG 286
QY 301 PRALFASVRPQGVVVAERDGRRLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL 360
Db 287 PSALFASVRPQGVVVAERGDRRLPAAVHVSVTLSREEAGAYAPLTAHGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGA 420
Db 347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTD-----GGGGGSIP-AAQSA 395
QY 421 ADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLLYHIGTWLLDSETHPLGMVAVKSS 437

RESULT 46
US-08-900-220C-10
; Sequence 10, Application US/08900220C
; Publication No. US20020045206A1
; GENERAL INFORMATION:
; APPLICANT: Miao, Ningning
; Wang, Monica
; Mahanthappa, Nagesh K.
; Pang, Kevin
; Jin, Ping
; TITLE OF INVENTION: Method of Treating Dopaminergic and
; GABA-nergic Disorders
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: ONE POST OFFICE SQUARE

APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,220C
FILING DATE: 24-Jul-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: ONV-044.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-900-220C-10

Query Match 73.2%; Score 1807; DB 8; Length 425;
Best Local Similarity 77.8%; Pred. No. 1.2e-149;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
4 MLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTILGASG 63
61 RYEGKISRNSERFKELTNPYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
64 RYEGKITRNSERFKELTNPYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123
121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
124 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 183
181 IHCSVKAENSVAAKSGGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
184 IHCSVKAENSVAAKSGGCPGSGATVHLEHGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 243
241 FLDRDDGAKKVFYVIETREPERERLLTAAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298
244 FLDRMDSSRKLFYVIETROPRARLLTAAHLLFVAPQHNQSEATG-----STSG----- 292
299 LGPRALFASRVPRGQRYVVAERDGRRLLPAAVHVS VTLSEEAAGAYAPLTAQGTILINR 358
293 ---QALFASNKPGQRYVVLGE--GGQQLLPASVHVS LREEASGAYAPLTAQGTILINR 347
359 VLASCYAVIEHSHWAHRAFAFPRLAHALLAALAPARTDRGDSGGGDRGGGGRVALTAP 418
348 VLASCYAVIEHSHWAHFAFPRLAQLGLAAL-----CP 381
419 GAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVAKSS 462
382 DGAIPATAATTTGIHWYSRLLYRIGSWVLDGDALHPLGMVAPAS 425

RESULT 47
US-08-954-771-8
; Sequence 8, Application US/08954771
; Publication No. US20030054437A1
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.

APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,771
FILING DATE: 20-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 04-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-954-771-8

Query Match 73.2%; Score 1807; DB 8; Length 425;
Best Local Similarity 77.8%; Pred. No. 1.2e-149;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
1 MLLARCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
4 MLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTILGASG 63
61 RYEGKISRNSERFKELTNPYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
64 RYEGKITRNSERFKELTNPYNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123
121 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180
124 KLRVTEGWDEDDGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 183
181 IHCSVKAENSVAAKSGGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
184 IHCSVKAENSVAAKSGGCPGSGATVHLEHGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 243
241 FLDRDDGAKKVFYVIETREPERERLLTAAHLLFVAP-HNDS-ATGEPEASSGSGPPSGGA 298
244 FLDRMDSSRKLFYVIETROPRARLLTAAHLLFVAPQHNQSEATG-----STSG----- 292
299 LGPRALFASRVPRGQRYVVAERDGRRLLPAAVHVS VTLSEEAAGAYAPLTAQGTILINR 358
293 ---QALFASNKPGQRYVVLGE--GGQQLLPASVHVS LREEASGAYAPLTAQGTILINR 347

QY 359 VLASYAVIEEHSWAHRAFPFRLAHALLAALAPARTDRGGSGGDRGGGGRVALTAP 418
Db 348 VLASYAVIEEHSWAHRAFPFRLAQGLLAAL-----CP 381
QY 419 GAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 382 DGAIPATAATTTTGIHWSRLYRIGSVWLDGDALHPLGMVAVPAS 425

RESULT 48
US-08-462-386D-8
; Sequence 8, Application US/08462386D
; Publication No. US20030186357A1
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Tissue Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,386D
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI-006CP3
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-386D-8

Query Match 73.2%; Score 1807; DB 8; Length 425;
Best Local Similarity 77.8%; Pred. No. 1.2e-149;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
QY 1 MLLARCLLVVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 4 MLLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTILGASG 63
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 64 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123
QY 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYVESKAH 180

Db 124 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYVESKAH 183
QY 181 IHCSVKAENSVAAKSGGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 184 IHCSVKAENSVAAKSGGCPGSGATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYSDFLT 243
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAP-HNDS-ATGEPEASSSGSPPSGGA 298
Db 244 FLDRMDSSRKLFYVETROPRARLLLTAAHLLFVAPQHNQSEATG-----STSG----- 292
QY 299 LGPRALFASVRPGRQVVVVAERDGRRLLPAAVHSVTLSSEAAAGAYAPLTAQGTILINR 358
Db 293 ---QALFASNKPGQRVYVIGE--GGQQLLPASVHSVSLREASGAYAPLTAQGTILINR 347
QY 359 VLASYAVIEEHSWAHRAFPFRLAHALLAALAPARTDRGGSGGDRGGGGRVALTAP 418
Db 348 VLASYAVIEEHSWAHRAFPFRLAQGLLAAL-----CP 381
QY 419 GAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGMVAVKSS 462
Db 382 DGAIPATAATTTTGIHWSRLYRIGSVWLDGDALHPLGMVAVPAS 425

RESULT 49
US-09-021-660A-34
; Sequence 34, Application US/09021660A
; Patent No. US20010041668A1
; GENERAL INFORMATION:
; APPLICANT: Baron, M.
; APPLICANT: Farrington, S.
; APPLICANT: Belausoff, M.
; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: HUIP-P01-060
; CURRENT APPLICATION NUMBER: US/09/021,660A
; PRIOR FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1997-02-10
; PRIOR APPLICATION NUMBER: 60/037,513
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049,763
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-021-660A-34

Query Match 73.2%; Score 1807; DB 9; Length 425;
Best Local Similarity 77.8%; Pred. No. 1.2e-149;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
QY 1 MLLARCLLVVSSLLVCSGLACGPGRGFKRRHPKLTPLAYKQFIPNVAEKTILGASG 60
Db 4 MLLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTILGASG 63
QY 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 120
Db 64 RYEGKITRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV 123
QY 121 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYVESKAH 180
Db 124 KLRVTEGWDEDEGHSESLHYEGRAVDITTSDDRRSKYGMRLARLAVEAGFDWVYVESKAH 183
QY 181 IHCSVKAENSVAAKSGGCPGSGATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 184 IHCSVKAENSVAAKSGGCPGSGATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYSDFLT 243
QY 241 FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAP-HNDS-ATGEPEASSSGSPPSGGA 298
Db 244 FLDRMDSSRKLFYVETROPRARLLLTAAHLLFVAPQHNQSEATG-----STSG----- 292

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|----|-----|--|-----|
| QY | 299 | LGPRALFASVRPGQRVVVAERDGRRLLPAAVHVSVTLSEEAAGAYAPLTAQGTILINR | 358 |
| Db | 293 | ---QALFASNVKPGQRVYLGE--GGQQLLPASVHVSLSREASGAYAPLTAQGTILINR | 347 |
| QY | 359 | VLASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAP | 418 |
| Db | 348 | VLASCYAVIEHSHWAHWAFAFRLAQGLLAAL-----CP | 381 |
| QY | 419 | GAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGMVKSS | 462 |
| Db | 382 | DCAIPTAATTTTGIHWYSRLLYRIGSWDLGDALHPLGMVAPAS | 425 |

RESULT 50

RESULT 50

US-09-151-999-10

; Sequence 10, Application US/09151999

; Patent No. US20020151460A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Elizabeth

; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE

; TITLE OF INVENTION: POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO

; FILE REFERENCE: ONV-031.02

; CURRENT APPLICATION NUMBER: US/09/151,999

; CURRENT FILING DATE: 1998-08-11

; EARLIER APPLICATION NUMBER: 08/955,552

; EARLIER FILING DATE: 1997-10-20

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 425

; TYPE: PRT

; ORGANISM: chicken Shh

US-09-151-999-10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 29, 2004, 18:28:04 ; Search time 20 Seconds
(without alignments)
2284.549 Million cell updates/sec

Title: US-09-883-848A-15
Perfect score: 2469
Sequence: 1 MLLARCLLLVSSLLVCS.....GMAVKSSXSRGAGGAREGA 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|--------|---------------|--------|----------|--------------------|
| 1 | 2062 | 83.5 | 437 | 2 A49425 | Sonic hedgehog pro |
| 2 | 2060 | 83.4 | 437 | 2 B53193 | hedgehog homolog v |
| 3 | 1807 | 73.2 | 425 | 2 A49424 | patterning protein |
| 4 | 1506 | 61.0 | 418 | 2 A53193 | hedgehog homolog v |
| 5 | 1498 | 60.7 | 444 | 2 S56765 | morphogen Xhh prec |
| 6 | 1459 | 59.1 | 415 | 2 A49426 | sonic hedgehog gen |
| 7 | 1183 | 47.9 | 396 | 2 B49425 | Desert hedgehog pr |
| 8 | 1027.5 | 41.6 | 336 | 2 C49425 | Indian hedgehog pr |
| 9 | 890 | 36.0 | 471 | 2 A46400 | segment polarity p |
| 10 | 449 | 18.2 | 94 | 2 G02735 | desert hedgehog - |
| 11 | 159.5 | 6.5 | 615 | 2 T29550 | hypothetical prote |
| 12 | 149 | 6.0 | 1207 | 2 T23754 | hypothetical prote |
| 13 | 138.5 | 5.6 | 1226 | 2 T24045 | hypothetical prote |
| 14 | 135.5 | 5.5 | 484 | 2 T34504 | hypothetical prote |
| 15 | 134.5 | 5.4 | 481 | 2 T27665 | hypothetical prote |
| 16 | 129 | 5.2 | 1147 | 1 MWAXIB | myosin heavy chain |
| 17 | 128 | 5.2 | 629 | 2 T19563 | hypothetical prote |
| 18 | 126.5 | 5.1 | 1021 | 2 T23252 | hypothetical prote |
| 19 | 123.5 | 5.0 | 2639 | 2 T31328 | fibroin - Chinese |
| 20 | 121 | 4.9 | 868 | 2 T22281 | hypothetical prote |
| 21 | 119 | 4.8 | 702 | 2 T35213 | probable secreted |
| 22 | 118.5 | 4.8 | 702 | 2 G01840 | T-box protein 2 - |
| 23 | 116 | 4.7 | 1329 | 2 E70917 | hypothetical glyci |
| 24 | 115.5 | 4.7 | 940 | 2 E87250 | [protein-PII] urid |
| 25 | 115 | 4.7 | 486 | 2 H87311 | hypothetical glyci |
| 26 | 114 | 4.6 | 741 | 2 G70917 | hypothetical glyci |
| 27 | 111 | 4.5 | 333 | 2 A39065 | homeotic protein E |
| 28 | 111 | 4.5 | 1298 | 1 EDBE75 | immediate-early pr |
| 29 | 110 | 4.5 | 462 | 2 T35852 | probable UDP-N-ace |

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|-----|-------|-----|------|----------|----------------------|
| 30 | 107.5 | 4.4 | 701 | 1 S46458 | transcription fact |
| 31 | 107 | 4.3 | 775 | 1 EDBE11 | immediate-early pr |
| 32 | 106.5 | 4.3 | 482 | 2 E70554 | hypothetical prote |
| 33 | 106 | 4.3 | 482 | 2 JC7583 | basic helix-loop-h |
| 34 | 105.5 | 4.3 | 490 | 2 T09084 | phosphatidylinosit |
| 35 | 105.5 | 4.3 | 841 | 2 C87331 | ISCC2, transposase |
| 36 | 105.5 | 4.3 | 1324 | 2 T14070 | peptide synthetase |
| 37 | 105.5 | 4.3 | 7463 | 2 T36248 | CDA peptide synthe |
| 38 | 105 | 4.3 | 460 | 2 T33110 | hypothetical prote |
| 39 | 104.5 | 4.2 | 510 | 2 A55207 | glycerol-3-phospha |
| 40 | 104 | 4.2 | 402 | 1 S25077 | monensin polyketid |
| 41 | 104 | 4.2 | 1063 | 2 A40253 | acidic nuclear pro |
| 42 | 104 | 4.2 | 3161 | 2 T30342 | protein HMWP1 - Ye |
| 43 | 103.5 | 4.2 | 975 | 2 S33121 | homeotic protein C |
| 44 | 102.5 | 4.2 | 413 | 2 E70661 | probable PE protei |
| 45 | 102.5 | 4.2 | 479 | 2 F70573 | hypothetical prote |
| 46 | 102.5 | 4.2 | 481 | 2 T27975 | hypothetical prote |
| 47 | 102 | 4.1 | 1145 | 2 B75625 | hypothetical prote |
| 48 | 102 | 4.1 | 1209 | 2 T00373 | hypothetical prote |
| 49 | 101.5 | 4.1 | 506 | 2 B84339 | hypothetical prote |
| 50 | 101.5 | 4.1 | 664 | 2 C70584 | probable serine-th |
| 51 | 101.5 | 4.1 | 777 | 2 C86454 | hypothetical prote |
| 52 | 101.5 | 4.1 | 1958 | 2 B40505 | hypothetical prote |
| 53 | 100.5 | 4.1 | 313 | 2 T15855 | hypothetical prote |
| 54 | 100.5 | 4.1 | 430 | 2 JC7379 | levansucrase (EC 2 |
| 55 | 100.5 | 4.1 | 2647 | 2 A37098 | gelation factor AB |
| 56 | 100 | 4.1 | 249 | 2 S41374 | single chain Fv an |
| 57 | 100 | 4.1 | 825 | 1 EDBEXD | immediate-early pr |
| 58 | 99.5 | 4.0 | 361 | 2 G70682 | hypothetical glyci |
| 59 | 99.5 | 4.0 | 598 | 2 T42070 | protein serine/thr |
| 60 | 99.5 | 4.0 | 874 | 2 B70945 | hypothetical prote |
| 61 | 99 | 4.0 | 244 | 2 T36357 | probable membrane |
| 62 | 99 | 4.0 | 758 | 2 A83121 | probable two-compo |
| 63 | 99 | 4.0 | 831 | 2 H84368 | MCM / cell divisio |
| 64 | 99 | 4.0 | 1022 | 2 T17406 | developmental prot |
| 65 | 98.5 | 4.0 | 867 | 2 S57795 | probable deoxyribo |
| 66 | 98 | 4.0 | 1061 | 2 A40609 | OmpA-related prote |
| 67 | 98 | 4.0 | 1376 | 1 VCBED6 | major capsid prote |
| 68 | 98 | 4.0 | 2129 | 2 T14182 | fxbC protein - Myc |
| 69 | 97.5 | 3.9 | 731 | 2 C70974 | hypothetical glyci |
| 70 | 97 | 3.9 | 519 | 2 A54590 | GAGA transcription |
| 71 | 97 | 3.9 | 808 | 2 F84038 | phenylalanyl-tRNA |
| 72 | 97 | 3.9 | 1010 | 2 I40329 | hypothetical prote |
| 73 | 97 | 3.9 | 1096 | 2 C87263 | hypothetical prote |
| 74 | 97 | 3.9 | 1541 | 2 T02831 | AAA protein I4171 |
| 75 | 96.5 | 3.9 | 341 | 2 C83578 | hypothetical prote |
| 76 | 96.5 | 3.9 | 410 | 2 JC7584 | basic helix-loop-h |
| 77 | 96.5 | 3.9 | 443 | 2 D87287 | pmbA protein limpo |
| 78 | 96.5 | 3.9 | 495 | 1 S31223 | transcription fact |
| 79 | 96.5 | 3.9 | 604 | 2 S25203 | srMR protein - Str |
| 80 | 96.5 | 3.9 | 930 | 2 T35180 | hypothetical prote |
| 81 | 96.5 | 3.9 | 1487 | 1 EDBEE1 | immediate-early pr |
| 82 | 96.5 | 3.9 | 1487 | 1 EDBEF6 | 155K transcription |
| 83 | 96 | 3.9 | 839 | 2 F75518 | hypothetical prote |
| 84 | 96 | 3.9 | 1017 | 2 F82500 | vgrG protein VCA01 |
| 85 | 96 | 3.9 | 1137 | 2 JC5950 | integrin alpha-7 c |
| 86 | 96 | 3.9 | 3163 | 2 T17440 | probable polyketid |
| 87 | 96 | 3.9 | 3163 | 2 AB0233 | yersiniabactin bio |
| 88 | 95.5 | 3.9 | 256 | 2 A70514 | hypothetical glyci |
| 89 | 95.5 | 3.9 | 431 | 2 S09824 | hypothetical prote |
| 90 | 95.5 | 3.9 | 461 | 2 T51044 | related to spore c |
| 91 | 95.5 | 3.9 | 475 | 2 A43915 | homeotic protein e |
| 92 | 95.5 | 3.9 | 497 | 2 F82985 | conserved hypothet |
| 93 | 95.5 | 3.9 | 756 | 2 T04187 | subtilisin-like pr |
| 94 | 95.5 | 3.9 | 908 | 2 A33280 | sarcolumenin precu |
| 95 | 95 | 3.8 | 419 | 2 AF1274 | tyrosyl-tRNA synth |
| 96 | 95 | 3.8 | 529 | 2 H84049 | hypothetical prote |
| 97 | 95 | 3.8 | 558 | 2 D69067 | succinate dehydrog |
| 98 | 95 | 3.8 | 577 | 2 AH2908 | hypothetical prote |
| 99 | 95 | 3.8 | 588 | 2 G97683 | prSD protein (U891 |
| 100 | 95 | 3.8 | 767 | 2 A35645 | major surface protei |
| 101 | 95 | 3.8 | 825 | 2 JC4163 | DNA-binding protei |
| 102 | 95 | 3.8 | 894 | 2 C86756 | prophage pi2 prote |

[illegible]

RESULT 6
A49426
sonic hedgehog gene shh protein - zebra fish
N;Alternate names: local cell-cell interaction signaling protein
C;Species: Brachydanio rerio (zebra fish)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C;Accession: A49426
R;Krauss, S.; Concordet, J.P.; Ingham, P.W.
Cell 75, 1431-1444, 1993
A;Title: A functionally conserved homolog of the Drosophila segment polarity gene hh is
A;Reference number: A49426; MUID:94094335; PMID:8269519
A;Accession: A49426
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-415 <KRA>
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:142459)
C;Superfamily: sonic hedgehog protein

| Query Match | 59.1%; | Score 1459; | DB 2; | Length 415; |
|-----------------------|------------------|---|------------|-------------|
| Best Local Similarity | 64.3%; | Pred. No. 6.4e-102; | | |
| Matches 295; | Conservative 47; | Mismatches 73; | Indels 44; | Gaps 6; |
| QY | 1 | M L L A R C L L L V S S L L V C S G L A C G P G R G F G K R R H P K L T P L A Y K Q F I P N V A E K T L G A S G | 60 | |
| Db | 1 | M R L L T R V L L S L I T L S L V S G L A C G P G R G Y G R R R H P K L T P L A Y K Q F I P N V A E K T L G A S G | 60 | |
| QY | 61 | R Y E G K I S R N S E R F K E L T P N Y N P D I I F K D E E N T G A D R L M T O R C K D K L N A L A I S V M N Q W P G V | 120 | |
| Db | 61 | R Y E G K I T R N S E R F K E L T P N Y N P D I I F K D E E N T G A D R L M T O R C K D K L N S L A I S V M N H W P G V | 120 | |
| QY | 121 | K L R V T E G W D E D G H H S E S L H Y E G R A V D I T T S D R D R S K Y C M L A R L A V E A G F D W V Y E S K A H | 180 | |
| Db | 121 | K L R V T E G W D E D G H H F E E S L H Y E G R A V D I T T S D R D K S K Y C T L S R L A V E A G F D W V Y E S K A H | 180 | |
| QY | 181 | I H C S V K A E N S V A A K S G G C F P G S A T V H L E Q G G T K L V K D L S P G D R V L A A D D Q G R L L Y S D F L T | 240 | |
| Db | 181 | I H C S V K A E N S V A A K S G G C F P G S A L V S L Q D G G Q K A V K O L N P G D K V L A A D S A G N L V F S D F I M | 240 | |

| | | | | |
|----|-----|-------------------|---|----------|
| QY | 241 | FLDRDDGAKKVFYV | IETREPERERLLLTAAHLLFVAHNDSATGEPEASSGGPPSGGALG | 300 |
| Dd | 241 | FTRDSTTRRVFYI | TQEPVEKITLTAHLLFVL---DNSTEDLHTMT----- | 286 |
| QY | 301 | PRLPFSRVRPGORVV | VVAERDCDRRLLPAAVHSVILSHEAAGAYAPLTAQGTLINRVL | 360 |
| Dd | 287 | --AAYASSVRAGOKVMV | ---DDSGQLKSIVIQRIYTEEQGSFAPVTAHGTVIVDRIL | 340 |
| QY | 361 | ASCVAVTIEHSWAHR | AFAPFRLAHALLAALAPARTDRGSDSCGDRGGGRVALTAPGA | 420 |
| Dd | 341 | ASCVAVIEDQGLAH | LAFAPARLYYYVSFLSP-KTPAVGPMRLYNRRGSTG---- | TPGS 394 |
| QY | 421 | ADAPGAGATAGIH | WYSQLLYQIGTWLLDSEALHPLGMV | 459 |
| Dd | 395 | C----- | HQMGTWLLDSNMLHPLGMSV | 415 |

RESULT 7
B49425
Desert hedgehog protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession: B49425
R;Echeillard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMa
Cell 75, 1417-1430, 1993
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implic
A;Reference number: A49425; MUID:94094334; PMID:7916661
A;Accession: B49425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <ECH>
A;Cross-references: GB:X76292; NID:G443941; PIDN:CAA53924.1; PID:G443942
C;Genetics:
A;Gene: Dhh
C;Superfamily: sonic hedgehog protein

| | Query Match | 47.9%; | Score 1183; | DB 2; | Length396; |
|----|-----------------------|--|--------------------|--------|----------------|
| | Best Local Similarity | 54.5%; | Pred. No. 3.3e-81; | | |
| | Matches | 244; | Conservative | 55; | Mismatches 87; |
| | | | | Indels | 62; |
| | | | | Gaps | 10; |
| QY | 3 | LLARCLLLVLVSSLLVCSGLACGPGRG-FGKRHPKK-LTPLAYKQFIPNVAEKTILGASG | 60 | | |
| Db | 7 | LLPLCCL-----ALLLSAQSCGPGRPVRRRYRKQLVPLLYKQFVPSMPERTILGASG | 61 | | |
| QY | 61 | RYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGV | 120 | | |
| Db | 62 | PAEGRVTRGSEFRDLVNPYNPDIIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV | 121 | | |
| QY | 121 | KLRVTEGWDEGHHSESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYESKAH | 180 | | |
| Db | 122 | RLRVTEGWDEGHHQAQSLHYEGRALDITTSDDRNKYGLLARLAVEAGFDWVYESRNH | 181 | | |
| QY | 181 | IHC5VKAENSVAAKSGGCPGCSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT | 240 | | |
| Db | 182 | IHSVKAADNSLAVRAGGCFGNATVRLRSGERKGLRELHRGWDVLAADAAGRVPVTPVLL | 241 | | |
| QY | 241 | FLDRDDGAKKVYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGP-PSGGAL | 299 | | |
| Db | 242 | FLDRDLQRRASFVAVETERPRKLLTTPWHLVFAA-----RGAPAPAGDF | 286 | | |
| QY | 300 | GPRALFASVRPQORVYVVAERDGDRLLLPAAVHSVTLSSEAAAGAYAPLTAQGTILINRV | 359 | | |
| Db | 287 | AP--VFARRLRAGDSVLA----PGGDALQPARVARVA-REEAVGVFAPLTAHGTLLVNDV | 339 | | |
| QY | 360 | LASCYAVIEEHSWAHRFAFPRFLAHALLAALAPARTDRGDSGGDRGGGGRVALTAPG | 419 | | |
| Db | 340 | LASCYAVLESHQWAHRFAFAPLRLLHALGALL-----PG | 372 | | |
| QY | 420 | AADAPGAGATAGIHWYSQLLYOIGTWLL | 447 | | |
| Db | 373 | GAVQP-----TGMHWYSRLLYRLABELM | 395 | | |

RESULT 8
C49425
Indian hedgehog protein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C/Accession: C49425
R/Echellard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMahon
Cell 75, 1417-1430, 1993
A/Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated
A/Reference number: A49425; MUID:94094334; PMID:7916661
A/Accession: C49425
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-336 <ECH>
A/Cross-references: GB:X76291
C/Superfamily: sonic hedgehog protein

Query Match 41.6%; Score 1027.5; DB 2; Length 336;
Best Local Similarity 54.6%; Pred. No. 1.3e-69;
Matches 218; Conservative 39; Mismatches 77; Indels 65; Gaps 8;

QY 71 ERFKELTPNPNPDIIFKDEENTGADRLMTQRCQKXKLNALAISVMNQWPGVKLRVTEGWDE 130
Db 1 ERFKELTPNPNPDIIFKDEENTGADRLMTQRCQKXKLNALAISVMNQWPGVKLRVTEGRDE 60

QY 131 DGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHHCYSVKAENS 190
Db 61 DGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVESKAHVHCSVKSEHS 120

QY 191 VAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFELTFLDRDDGAKK 250
Db 121 AAATGGCFPAGAQVRLNGERVALSAVKPGDRVLAMGEDGTPTFSDVLIIFLDREPRLR 180

QY 251 VFYVIETREPRERILLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALFASRVR 310
Db 181 AFQVIETQDPPRRLLTPAHLFLIA--DNHT-EPAAHF-----RATFASHVQ 224

QY 311 PQQRVYWAERDGRLLPAAVHVSITLSEEAAGAYAPLTAQGTILINRVLASCYAVIEEH 370
Db 225 PQQYVLV---SGVPGLOPARVAVS-THVALGSYAPLTRHGTLLVVEDVVASCFAAVADH 279

QY 371 SWAHRAFAFRLAHALL-AAALAPARTDRGGSGGDRGGGGRVALTAPGAADAPGAGAT 429
Db 280 HLAQLAFWPLRLFPPLAWSWTPE-----D----- 304

QY 430 AGIHWYSQLLYQIGTWLLDSEALHPLGMVKSXSRGAG 468
Db 305 -GVHSYPQMLYRLGLRLLEESTFHPGLMS-----GAG 335

RESULT 9
A46400
segment polarity protein hedgehog - fruit fly (Drosophila melanogaster)
N/Alternate names: hh protein
C/Species: Drosophila melanogaster
C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C/Accession: A46400; JN0501; A43480
R/Tabata, T.; Eaton, S.; Kornberg, T.B.
Genes Dev. 6, 2635-2645, 1992
A/Title: The Drosophila hedgehog gene is expressed specifically in posterior compartment
A/Reference number: A46400; MUID:94040725; PMID:1340474
A/Accession: A46400
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-471 <TAB>
A/Cross-references: GB:S66384; NID:G435848; PID:G435849
A/Experimental source: Oregon-R
A/Note: sequence extracted from NCBI backbone (NCBIN:138996, NCBI:P:138997)
R/Tashiro, S.; Michiue, T.; Higashijima, S.; Zenno, S.; Ishimaru, S.; Takahashi, F.; Ori
Gene 124, 183-189, 1993
A/Title: Structure and expression of hedgehog, a Drosophila segment-polarity gene requir
A/Reference number: JN0501; MUID:93185922; PMID:8166882

A/Accession: JN0501
A/Molecule type: mRNA
A/Residues: 1-471 <TAS>
A/Cross-references: GB:L05404
A/Note: it is uncertain whether Met-1 or Met-51 is the initiator
A/Note: intron positions were determined from partial DNA sequence
R/Lee, J.J.; von Kessler, D.P.; Parks, S.; Beachy, P.A.
Cell 71, 33-50, 1992
A/Title: Secretion and localized transcription suggest a role in positional signaling f
A/Reference number: A43480; MUID:93008241; PMID:1394430
A/Accession: A43480
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-471 <LEE>
A/Cross-references: GB:L02793; NID:G157609; PID:G157610
A/Note: sequence extracted from NCBI backbone (NCBI:P:115418)
C/Comment: This protein is required for cell-cell communication.
C/Genetics:
A/Gene: hh
A/Cross-references: FlyBase:FBgn0004644
A/Introns: 160/3; 248/1
C/Superfamily: sonic hedgehog protein
C/Keywords: transmembrane protein
F/62-82/Domain: transmembrane #status predicted <TMM>

Query Match 36.0%; Score 890; DB 2; Length 471;
Best Local Similarity 44.3%; Pred. No. 4.2e-59;
Matches 202; Conservative 65; Mismatches 137; Indels 52; Gaps 10;

QY 6 RCL-----LLVYSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIG 57
Db 59 RCLSRLTSLVALLLVLPMVFPSPAHSCGPGRGLGRHR-ARNLYPLVLKQITIPNLSEYTN 117

QY 58 ASGRYEGKISNRSEPKELTPNPNPDIIFKDEENTGADRLMTQRCQKXKLNALAISVMNQW 117
Db 118 ASGPLEGVIRRDSPKFDLPNPNRDILFRDEEGTGADRLMSKRCCKEKLNLVLAISMNEW 177

QY 118 PGVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYVES 177
Db 178 PGIRLLVTEGWDEYHGHQESLHYEGRAVTIATSDRDQSKYGMRLARLAVEAGFDWVSYS 237

QY 178 KAHHCYSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYS 237
Db 238 RHHYCSVKSDSSISSHVHGCFTPESTALLESQVGRKPLGELSIGDRVLSMTANGQAVYSE 297

QY 238 FLTFLDRDDGAKKVFYVETREPRERILLTAHLLFVAPHNDSATGEPEASSGSGPPSGG 297
Db 298 VILFMDRNLEQMNFVQLHT-DGGAVLTVTPAHLVSV-----WQPESQKLT----- 342

QY 298 ALGPRALFASRVRPQQRVYVAERDGRRLPAAVHVSITLSEEAAGAYAPLTAQGTILIN 357
Db 343 -----FVFADRIEKNQVLRDVTETELR--PQRVVKVG-SVRSKGVVAPLTREGTIWN 394

QY 358 RVLASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGGSGGDRGGGGRVALTA 417
Db 395 SVAASCYAVINSQSLAHWGLAPMRLSLTLEAWL-PAKEQ-----LHSS 436

QY 418 PGAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALH 453
Db 437 PKVYSS--AQQONGIHWYANALYKVKDYVLPQSNRH 470

RESULT 10
G02735
desert hedgehog - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 11-Jan-2000
C/Accession: G02735
R/Drummond, I.A.
submitted to the EMBL Data Library, June 1996
A/Reference number: H01643
A/Accession: G02735
A/Status: preliminary; translated from GB/EMBL/DBJ

Db 1114 -----AIFASDLEVGDCVVVLYKGYRQKIETITRSV-----RTGIYSPLTNNGRII 1161

QY 356 INRVLASCYAVIEHS-----WAH 374

Db 1162 VNDMLASCYSEIQNTLQTTFFWAY 1186

RESULT 14

T34504

hypothetical protein ZK1290.12 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T34504

R;Taich, A.

submitted to the EMBL Data Library, July 1995

A;Description: The sequence of C. elegans coamid ZK1290.

A;Reference number: Z21535

A;Accession: T34504

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-484 <TAI>

A;Cross-references: EMBL:U21308; PIDN:AAB93321.1; GSPDB:GN00020; CESP:ZK1290.12

A;Experimental source: strain Bristol N2; clone ZK1290

C;Genetics:

A;Gene: CESP:ZK1290.12

A;Map position: 2

A;Introns: 66/3; 124/2; 181/2; 392/1

Query Match 5.5%; Score 135.5; DB 2; Length 484;

Best Local Similarity 24.5%; Pred. No. 0.021;

Matches 46; Conservative 42; Mismatches 65; Indels 35; Gaps 8;

QY 191 VAAKSGCFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLFLD 250

Db 283 VASGVPACFTGNSKV-MTPAGEKSMADLSVGMVMTY-EYGRMTYTRVASWLHRLPDTKA 340

QY 251 VFYVETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGALGPRALFASRVR 310

Db 341 AFIKL-TTEQGAIIDMTPQHFIYKA---NCVTEEME-----LVYAEDMT 380

QY 311 PQQRVVVVAERDGRLLPAAVHVSVTLSEEA-----AGAYAPLTAQGTILINRVLASCYAV 366

Db 381 IGDCLMV---KENEKLVM-----TTISEKSTFYETGVYAPMTETGDLIVDDVYASCHNV 431

QY 367 IEHSHWAH 374

Db 432 VKANTLSH 439

RESULT 15

T27665

hypothetical protein ZK1037.10 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T27665

R;Basham, V.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z20401

A;Accession: T27665

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-481 <WIL>

A;Cross-references: EMBL:Z81142; PIDN:CAB03509.1; GSPDB:GN00023; CESP:ZK1037.10

A;Experimental source: clone ZK1037

C;Genetics:

A;Gene: CESP:ZK1037.10

A;Map position: 5

A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3

Query Match 5.4%; Score 134.5; DB 2; Length 481;

Best Local Similarity 24.3%; Pred. No. 0.024;

Matches 45; Conservative 34; Mismatches 67; Indels 39; Gaps 6;

QY 198 CFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLFLD-----RDDGAKKVF 252

Db 314 CFPNDAVVNVYEKAVKRMDLEIGDWVEALDENG-----EDITFLPVKYLWHRDPEQAE 368

QY 253 YVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGALGPRALFASRVRPF 312

Db 369 FLEFSLDNGETFTLTKHLVY-----TTECRQNS-----SELKISWESISAGKVNAG 415

QY 313 QRVVVAERDGRLLPAAVHVSVTLSE-----EAAGAYAPLTAQGTILINRVLASCYA 365

Db 416 DCFYLAQSE-----ALTKYRLVEILDIKRVKKTGIYAPMTSQGHLLVNKIHTSCHS 466

QY 366 VIEEH 370

Db 467 EVDHH 471

RESULT 16

MWAXIB

myosin heavy chain IB - Acanthamoeba castellanii

N;Contains: myosin ATPase (EC 3.6.4.1)

C;Species: Acanthamoeba castellanii

C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 19-Apr-2002

C;Accession: JQ0095; B34448

R;Jung, G.; Schmidt, C.J.; Hammer III, J.A.

Gene 82, 269-280, 1989

A;Title: Myosin I heavy-chain genes of Acanthamoeba castellanii: cloning of a second ge

A;Reference number: JQ0095; MUID:90060816; PMID:2511079

A;Accession: JQ0095

A;Molecule type: DNA

A;Residues: 1-1147 <JUN>

A;Cross-references: GB:M30780

A;Note: this organism expresses at least three isoforms of myosin I heavy-chain, encode

of gene MIB, whereas the protein previously identified as MIB is the product of gene MI

R;Brzeska, H.; Lynch, T.J.; Martin, B.; Korn, E.D.

J. Biol. Chem. 264, 19340-19348, 1989

A;Title: The localization and sequence of the phosphorylation sites of Acanthamoeba myo

A;Reference number: A34448; MUID:90037074; PMID:2530230

A;Accession: B34448

A;Molecule type: protein

A;Residues: 538-550, 'X', 552-559 <BRZ>

C;Comment: In this protein, the coiled-coil rod-like region found in many myosin heavy

protein is globular and does not self-assemble into filaments.

C;Genetics:

A;Gene: MIB

A;Introns: 1/3; 39/3; 102/2; 135/3; 183/3; 212/1; 291/3; 379/3; 492/3; 617/2; 649/3; 78

C;Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homol

C;Keywords: actin binding; ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein;

F;12-664/Domain: myosin motor domain homology <MMOT>

F;103-110/Region: nucleotide-binding motif A (P-loop)

F;552-573/Region: actin binding #status predicted

F;698-1147/Domain: carboxyl-terminal <CTD>

F;698-889/Region: basic

F;910-1094/Region: alanine/glycine/proline-rich

F;1097-1144/Domain: SH3 homology <SH3>

F;109/Binding site: ATP (Lys) #status predicted

F;315/Binding site: phosphate (ser) (covalent) #status predicted

Query Match 5.2%; Score 129; DB 1; Length 1147;

Best Local Similarity 21.3%; Pred. No. 0.19;

Matches 104; Conservative 55; Mismatches 180; Indels 150; Gaps 21;

QY 44 YKQITPNVAEKTILGASGRYEGKISRNSERFKELTNNYNDIIFKD---EENTGADRLMT 99

Db 591 YLGLLENVVRVRRAGFA--YRAEFDRFLRRYKKLSP-----KTWGIWGENSGAPK--- 637

QY 100 QRCKDKLNALAISVMNQWPGVKLRVTEGWDEGDGHSESL-----HYEG 143

Db 638 DGCQTLLNDLGLDT-SQWLCKSKVFIRYPETLFLHEECLDRKYDYDCTLRIOKAWRHWS 696

QY 144 R-----AVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAK 194

Db 697 RKHQLERQKMAADLLKGGKERQHSVNRKYE---FDYINYDANYPLQDCVR---SSGRDK 750

QY 195 SGGCPGSA TVHLEQGGTKLVKDLSPGDRVLAADDQGR-----LLYSDFLTFLLDRDDGA 248
Db 751 EATAFT-----DQVLVLRNRGKPERRDLIIVTNEAVFAMRKKKS 789
QY 249 KKVFYVIEPREPRERLLLTAAHLL---FVAPH-----NDSATGEPEASSGSGPPSG 296
Db 790 GQVVYNLKRRIPLGEIASLSLSTLQDNYVVIHNNQYDMVFENDKKTEIVTILMENYKMSG 849
QY 297 GALGPRALFASRVPRGQRVVYVAERDGDRLLLPAAVHSVLTSEEAAGAYAPLTAQGTILI 356
Db 850 GRDLP-----VNFNDNITYKASNGAQRRL-----TFSKNESASAQPSIKKS---- 890
QY 357 NRVLASCYAVIEHSHWAHRAFAFAPRLAHALLAALAPARTDR-----GGDSGGGDR 406
Db 891 -----RANIQIGIATGL-----PKETDSSPPNWTSPSGGGGGYGGGRG 927
QY 407 GGGGRRVALTAPGAADAPGAGATAGIHWSYQLLYQIGTWLLDSEALHPLGMVKSXSXSRG 466
Db 928 GGGGGRGA--AGGGRGGFGGGGGG--YSQPVQA-----AQPVAQVPQPVAAVPSAGRG 977
QY 467 AGGGAREGA 475
Db 978 GPGMGGPGA 986

RESULT 17

T19563
hypothetical protein C29F3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T19563; T23034
R;Matthews, L.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19142
A;Accession: T19563
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-629 <WIL>
A;Cross-references: EMBL:Z81043; PIDN:CAB02804.1; GSPDB:GN00023; CESP:C29F3.2
A;Experimental source: clone C29F3
R;White, S.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z19657
A;Accession: T23034
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-629 <WI2>
A;Cross-references: EMBL:AL023813; PIDN:CAA19424.1; GSPDB:GN00023; CESP:C29F3.2
A;Experimental source: clone H02K04
C;Genetics:
A;Gene: CESP:C29F3.2
A;Map position: 5
A;Introns: 23/1; 111/3; 207/2; 287/1; 381/3; 399/3; 417/1; 476/2; 528/3; 537/2; 5

Query Match 5.2%; Score 128; DB 2; Length 629;
Best Local Similarity 24.6%; Pred. No. 0.11;
Matches 43; Conservative 35; Mismatches 75; Indels 22; Gaps 7;
QY 198 CFFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLDRD--DGAKKVFYVI 255
Db 421 CFPADAENVYERGVKRMDELEVGDWVQALHGK-ETTYSPVKYWLHRDPEQAEFVEFL 479
QY 256 ETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALFASRVPRGQV 315
Db 480 EN--GESFTLTKHLVFATDCQONVKNLDDLN---PTSTG-----KINIGE-C 521
QY 316 YVVAERDGDRLLLPAAVHSVLTSEEAAGAYAPLTAQGTILINRVLASCYAVIEEH 370
Db 522 FFMAQPENASKFQVQILDIQVRK-TGIYAPMTSLGHLNVNQIHTSCHSEIDHH 575

RESULT 18

T23252
hypothetical protein K02E2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23252
R;Lloyd, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19716
A;Accession: T23252
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1021 <WIL>
A;Cross-references: EMBL:Z81560; PIDN:CAB04547.1; GSPDB:GN00023; CESP:K02E2.2
A;Experimental source: clone K02E2
C;Genetics:
A;Gene: CESP:K02E2.2
A;Map position: 5
A;Introns: 41/1; 79/3; 131/3; 197/1; 262/1; 297/3; 566/3; 610/3; 735/3; 775/3; 834/3; 88

Query Match 5.1%; Score 126.5; DB 2; Length 1021;
Best Local Similarity 27.1%; Pred. No. 0.26;
Matches 52; Conservative 34; Mismatches 65; Indels 41; Gaps 10;
QY 198 CFFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLDRDDGAKKVFYVIET 257
Db 802 CFSRDTWV-TTPSGKKRMDEIBIGDYVLTADLK-TALFSAITLWIHREPETVQEFLEIKT 859
QY 258 REPRERLLTAAHLLFVA-----PHNDS---ATGE-----PEASSGSGPPSGGAL 299
Db 860 -DNGKTLQLTAGHFIYATECRYLPKSNSSLLNSTPERYRHLIDTLPDDS----- 907
QY 300 GPRALFASRVPRGQRVVYVAERDGDRLPAAVHSVLTSEEAAGAYAPLTAQGTILINR 358
Db 908 --ETKLASQLKIGECLLI--HNGQFRMQKIDSISKIVS---TGIYSPLTENGRIIVND 959
QY 359 VLASCYAVIEEH 370
Db 960 VLASCYSEVQQN 971

RESULT 19

T31328
fibroin - Chinese oak silkmoth
C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31328
R;Sezutsu, H.; Tamura, T.; Yukuhiro, K.
submitted to the EMBL Data Library, August 1998
A;Description: Characterization of the full length fibroin gene of a wild silkworm, Antt
A;Reference number: Z20995
A;Accession: T31328
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2639 <SEZ>
A;Cross-references: EMBL:AF083334; NID:G3450882; PID:G3450883; PIDN:AAC32606.1
C;Genetics:
A;Introns: 14/3

Query Match 5.0%; Score 123.5; DB 2; Length 2639;
Best Local Similarity 28.5%; Pred. No. 1.5;
Matches 55; Conservative 10; Mismatches 101; Indels 27; Gaps 6;
QY 280 SATGEPEASSGSGPPSGGALGPRALFASRVPRGQRVYVVAERDGDRLPAAVHSVLTSE 339
Db 2167 AAAAAAAGSGAGRGDGGYGSG---SSAAAAAARRACHERAAGSAA----- 2216
QY 340 EAAGAYAPLTAQGTILINRVLASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGG 399
Db 2217 -AAAAAASGA---GRSGGS-----YGVGDGGYGSDSAAAAAASGAGG 2265
QY 400 DSGGGDRGGGG--GRVALTAPGAADAPGATAGIHWSYQLLYQIGTWLLDSEALHPLGM 457
Db 2266 SGGYGGYGGYGSDSAAAAAASGAGGAGGYGGYG---GYSGYGSDSAAAAAAA 2321

QY 458 AVKSSXSRGAGGG 470
Db 2322 AAAGSGAGGVGGG 2334

RESULT 20
T22281
hypothetical protein F46B3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22281
R;Alnscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19541
A;Accession: T22281
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-868 <WIL>
A;Cross-references: EMBL:Z81540; PIDN:CAB04405.1; GSPDB:GN00023; CESP:F46B3.5
A;Experimental source: clone F46B3
C;Genetics:
A;Gene: CESP:F46B3.5
A;Map position: 5
A;Introns: 45/3; 200/1; 235/3; 436/3; 561/3; 581/3; 696/3; 742/1; 826/3; 846/3

Query Match 4.9%; Score 121; DB 2; Length 868;
Best Local Similarity 26.7%; Pred. No. 0.54;
Matches 47; Conservative 32; Mismatches 73; Indels 24; Gaps 8;

QY 196 GGCFFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLDRDDGAKKVFYVI 255
Db 662 GGCFF-SSDTLVTPSGKKRMDEIDVG DYVLT A-NRVKTHFTPTVLWIHRESEKLEEFLLI 719

QY 256 ETREPRERLLITAAHLLFVAPHNDSATG---EPEASSGSGPPSGGALGPRALFASRVRP 312
Db 720 -TTERGSTLQTLPLHFMYRTKCNESSEFLKILPE-----NHEAILASYLEIG 765

QY 313 QRVVVAERDGDRLLPAAVHVS VTLSEEAAGAYAPLTAQGTILINRVLASCYAVIE 368
Db 766 DCV-ILTENTKFRQ---EKNQTTIRGLK-TGIYSPLTKNGRIIVNDMLASCYSEVQ 816

RESULT 21
T35213
probable secreted protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35213
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21572
A;Accession: T35213
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-318 <SEE>
A;Cross-references: EMBL:AL031515; PIDN:CAA20618.1; GSPDB:GN00070; SCOEDB:SC5C7.06
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5C7.06

Query Match 4.8%; Score 119; DB 2; Length 318;
Best Local Similarity 26.3%; Pred. No. 0.21;
Matches 59; Conservative 19; Mismatches 100; Indels 46; Gaps 9;

QY 276 PHNDSATGEPEASSGSGPPSGGALGPRALFASRVRPQORVVVVAERDGDRLLPAAVHSV 335
Db 46 PADDSAAVPPPSAEAEAPPSPACQAAAR-VSPSDAGFGDTTV-----SV 88

QY 336 TLSEEAAGAYAPLTA-----QGTILINRVLASCYAVIEHSHWAHRAFAFRLAHALLAA 389
Db 89 SCGPTGGSAPASLDATSAAFEGTVLRKVADTAGTA---SGPAYRGTARIAAEEDFAAE 145

QY 390 LAPARTDRGGDSGGDRGGGGRVALTAPGAADAPGAGAT-----AGIHWYSQL--LYQI 442
Db 146 RPPADITDPG--GATDPEGAANPEGATAPGSATDPGGVATDGEPSAGTEGWAETGDSABA 203

QY 443 G-TWLLDSEALHPLG-----MAVKSSXSRGAGGGAREGA 475
Db 204 GDDWTVDGACPDASGGEGDPWSATMSVPEESGAGAGAGAAQPA 247

RESULT 22
G01840
T-box protein 2 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: G01840
R;Campbell, C.E.
submitted to the EMBL Data Library, May 1995
A;Reference number: G08602
A;Accession: G01840
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-702 <CAM>
A;Cross-references: EMBL:U28049; NID:G924927; PIDN:AAA73861.1; PID:G924928
C;Genetics:
A;Gene: GDB:TBX2
A;Cross-references: GDB:568496; OMIM:600747
A;Map position: 17q21-17q22
C;Superfamily: mouse transcription factor tbx2; T-box homology
F;104-285/Domain: T-box homology <TBX>

Query Match 4.8%; Score 118.5; DB 2; Length 702;
Best Local Similarity 19.3%; Pred. No. 0.63;
Matches 116; Conservative 46; Mismatches 144; Indels 295; Gaps 23;

QY 118 PGVKLRVTEGWDEGHHSEESLHYEGRAVDITTSDR-----DRSKYGM LAR 163
Db 95 PKVTLEAKELWDQ-----FHKLGTEMVITKSGRRMFPFFKVRVSGLDKKAKYILL-- 144

QY 164 LAVEAGFDWVYVESKAHHC SVKAENS---VAAKSGGCGFP GSATVHLEQGGT----- 212
Db 145 MDIVAADD-----CRYKFHNSRMVMVAGKADPEMPKRMVTHPDS PATGEQWMAKP 193

QY 213 -----KLVKOLS-----PGRVLAADDQGRLLYSDFLFL----- 242
Db 194 VAFHKLKLTNNISDKHGFTILNSMHKYQPRFHVIRANDILKLPYSTFRIVVFPETDFIAV 253

QY 243 -----DRDDGAKKVFVVIETREPRERLLLTAAHLL--FVAPHND 279
Db 254 TAYQNDKITQLKIDNPNPAKGFRTDNGR-----REKRQLTLP SLRLYEEHCKPERD 306

QY 280 SATGEPEASSGSGPPS-----GGALGPRALFASRV----- 309
Db 307 GA--ESDASSCDPPPARBPPTSPGAAPSLRLHRAAEKSCAADS DPPERLSEERARA 364

QY 310 -----RPGQRVVVAERDGD-----RR----- 326
Db 365 PLGRSPAPDSASPTRLTEPERARERRC PERGKEPAESGGDGPFG LRSLEKERPEAR KDE 424

QY 327 -----LLPAAVHSVTLSEEAAG-----AYAPLTAQGTILINRV 359
Db 425 GRKEAEGKEQGLAPLVVQTD SASPLGAGHLPG LAFSSHLHGQQFFG PLGAGQPLFLHP- 483

QY 360 LASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGGDSGGGDRGGGRVALTAPG 419
Db 484 -----GQFTMGPGAFSAMGMGH-LLASVA-----GGNGGG--GGPGTAAGLDAGG 526

QY 420 AADAPGAGATAG---IHWYSQL----- 439
Db 527 LGPAASAASTAAPFPFHL SQHMLASQGI PMPTFGGLFPYPYTYMAAAAAAASALPATSAA 586

QY 440 -----YQIGTWLLDSEALHPLGMVKSXSRGAGGGAR 472
Db 587 AAAAAAGSLSRPFLG SARPRLRFSPYQIPVTIPPSLLTTGLA--SEGSKAAGNSR 644

| | | |
|----|-------|-----|
| QY | 473 E | 473 |
| | | — |
| Dp | 645 E | 645 |

RESULT 23
E70917
Hypothetical glycine-rich protein Rv1450c - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C.Accession: E70917
R.; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A.Reference number: A70500; MUID:98295987; PMID:9634230
A.Accession: E70917
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-1329 <COL>
A.Cross-references: GB:Z95844; GB:AL123456; NID:G3250713; PIDN:CAB09271.1; PID:G2131046
A.Experimental source: strain H37RV
C.Genetics:
A.Gene: Rv1450c
C.Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

```
Query.Match      4.7%; Score 116; DB 2; Length 1329;
Best Local Similarity 28.3%; Pred. No. 2.2;
Matches 68; Conservative 18; Mismatches 90; Indels 64; Gaps 12;
```

| | | | |
|----|-----|---|-----|
| QY | 271 | LLFVAPHNDSATGEPEASSGS--GPPSGGALGP-----RALFASRVVRPG | 312 |
| Db | 3 | LVIVAPETVAAALDVARIGSSIGAAANAAGSTTSVLAAGADEVSAAIATLFGSHAREY | 62 |
| QY | 313 | QRV--YVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCVAVIEEH | 370 |
| Db | 63 | QAISTQVAAFHDRFAQTLTSAAVGSY-VSAEATNA-APLATLEHNVLNALNAPTQAL---- | 116 |
| QY | 371 | SWAHRAFAFRLAHALL--AALAPARTDRGDSGG-----GDRGGGGGRV | 413 |
| Db | 117 | -----LGRPLIGDGAAGAPG-TQAGGAGGILWNGGAGSGSGAPQVVGAGGAA | 164 |
| QY | 414 | ALTAP-GAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPL-GMAVKSSXSRGAGGGA | 471 |
| Db | 165 | GLFGTGGAGGACGAGAAGGAG-----GSGGWLILNGGVGGAGGOSLLGGATGAGGNA | 217 |

RESULT 24
E87250
[protein-pII] uridylyltransferase [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 02-Jun-2003
C/Accession: E87250
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: E87250
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-940 <STO>
A/Cross-references: GB:AE005673; NID:g13421101; PIDN:AAK22001.1; GSPDB:GN00148
C/Genetics:
A/Gene: CC0013
C/Superfamily: UTP:GlnB (protein PII) uridylyltransferase

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|-----------------------|-------|----------------|-------|-------------|
| Query Match | 4.7% | Score 115.5; | DB 2; | Length 940; |
| Best Local Similarity | 23.2% | Pred. No. 1.5; | | |

| | Matches | 82; | Conservative | 39; | Mismatches | 155; | Indels | 77; | Gaps | 14; |
|----|---------|---|--------------|-----|------------|------|--------|-------|------|-----|
| QY | 90 | ENTGADRLMTQRCKDKLNALAISVMNQWFGVKLRVTEGWDEDDGHSEESLHYEGRAVDIT | : | : | : | : | : | : : : | : | 149 |
| Dd | 610 | ENPERLLLVITTVADIRAVGPVGWNGWKQLLR-----ELYNATEAVFRGGRGSDAA | : | : | : | : | : | : : : | : | 662 |
| QY | 150 | TS-DRDRSKYGMRLARLAVERAGFDWYYYESKAHHCVSVAENSVAAKSGGCFPGSAT---- | : | : | : | : | : | : | : | 204 |
| Dd | 663 | ANVRHQESTABAAAAL-----LETPPAKKGWVAAMENAYFSAFSQDDL F | : | : | : | : | : | : | : | 708 |
| QY | 205 | VHLE-----QGGTKLVKDLSPGDR---VLAADDDQGRLLYSDFL----- | : | : | : | : | : | : | : | 239 |
| Dd | 709 | HHAELARRAIIQGGAAAEQVRPGSNAAEVVTAADR-RGLFADLALAISSLGNVVUGAR | : | : | : | : | : | : : : | : | 767 |
| QY | 240 | TFLDRDDGAKKVFFVIE-TREP----RERLLLTAHHLLFEVAPHNDSATGEPEASSSGSGPP | : | : | : | : | : | : | : | 294 |
| Dd | 768 | VFTSRQGOALDVFYVQDVGTGAPFGCENPRALRRLLADALEAAGKGDALAVEPRRRGSEQTRA | : | : | : | : | : | : : : | : | 827 |
| QY | 295 | SGGALGPRALF-----ASRVRPQGVVVVVAERDGD RRLLLPAAVHSVTLSEE | : | : | : | : | : | : | : | 341 |
| Dd | 828 | AFAIAPSVTIIDNASNDATVVEASGRDRPG-LHLAKTLDADSALSIOQSAHIDGYGERA | : | : | : | : | : | : | : | 886 |
| QY | 342 | AGAYAPLTAQG-----TILINRVLASCYAVIEEHSWAHRAFAP-FRLAHALLA | : | : | : | : | : | : | : | 388 |
| Dd | 887 | VDAFYVOTTEGGKVTDTRKLNALKADLLAALQEONASAPAARPGLRRRARASVA | : | : | : | : | : | : | : | 939 |

RESULT 25
H87311
hypothetical protein CC0505 [imported] - *Caulobacter crescentus*
C/Species: *Caulobacter crescentus*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change
C/Accession: H87311
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; V
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

| | | | | |
|-----------------------|------------------|-----------------|------------|-------------|
| Query Match | 4.7%; | Score 115; | DB 2; | Length 486; |
| Best Local Similarity | 21.7%; | Pred. No. 0.71; | | |
| Matches 85; | Conservative 50; | Mismatches 170; | Indels 86; | Gaps 17; |

| | | | |
|----|-----|---|-----|
| QY | 111 | ISVMNQPGVKLRVTGWEDEGHHS--EESLHYEGRAV---DITTSDDRRDSKYGMLARLAV | 166 |
| Db | 1 | METMRAWTGLVLAITLGIWIAPAHAAPASAPAKARLIVLSDIENEPDDTQSFVRLLYAN | 60 |
| QY | 167 | EAGFDWVYVESKAHTHCSVKAEN--SVAAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRV | 224 |
| Db | 61 | EIDIEALVATTSTHVRGEIHPEsirRLVSLYGQVRP--NLVLHANGYPTAESLSARIRA | 117 |
| QY | 225 | -----LAADDQGRLLYSDFLTFLDRDDGAKKVFYVIETREPRERLLLT--AAHLLFVAP | 276 |
| Db | 118 | GQPAYGLAATGPK-----DTEGSRAIIAALDSPDPRPVWVSVWGGANTLAQAL | 166 |
| QY | 277 | HNDSATGEPEASSGSGPPGCGALGPRALFASRVRPQORVYVVAERDGD---RRLLPAAV | 332 |
| Db | 167 | KTLEAT-RPAAE-----VQRLISKLRVVTISDQDDAGAWIRKTYPSLF | 208 |
| QY | 333 | HSVTLSEEAAGAYAPLTAQGTI-----LINRVLASCY-----AVIEEHSWAH | 374 |
| Db | 209 | YIV-----SPGGYGAAATWGGIFQAVDGLDNTTVSNAWLAQNIOQGRGPLGAAYPDVAYGM | 263 |
| QY | 375 | RAFAPFRLAHALLAALAPARTDRGGDSGGDRGGGGRVALTAPGAADAPGAGATAGIHW | 434 |

Db 264 EGDTPAFL-NLIPTGLA-----DPERPDWGGWGRVALYTPNLADTPKGTGGVPI 314

QY 435 YSOLLVOICTWLLDSEALH---PLGMAVKSS 462

Db 315 EPE-TRPIWTNAIDTVAPHEPAPFGRAVKVS 344

RESULT 26

G70917

hypothetical glycine-rich protein Rv1452c - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003

C;Accession: G70917

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: G70917

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-741 <COL>

A;Cross-references: GB:Z95844; GB:AL123456; NID:G3250713; PIDN:CAB09269.1; PID:G2131044

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv1452c

C;Superfamily: elastin related uncharacterized glycine-rich protein, PE motif containing

Query Match 4.6%; Score 114; DB 2; Length 741;

Best Local Similarity 27.9%; Pred. No. 1.5;

Matches 67; Conservative 18; Mismatches 91; Indels 64; Gaps 12;

QY 271 LLFVAPHNDSATGEPEASSGS--GPPSGGALP-----RALFASRVPRG 312

Db 3 LVIVTPETVAASDVARISSIGVANSAAAGSTTSVLAAGADEVSAAIATLFGSHAREY 62

QY 313 QRV--YVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYAVIEEH 370

Db 63 QAISTQVAAFHDFPAQTLSAAVGSY-VSAEATNA-APLATLEHNVNLNAPTQAL---- 116

QY 371 SWAHRAFAFRLAHALL---AALAPARTDRGDSGG-----GDRGGGGGRV 413

Db 117 -----LGRPLIGDGAAGAPG-TGAGGAGGILWNGGGAGSGGAPGVGGAGGAA 164

QY 414 ALTAP-GAADAPGACATAGIHWSQLLYQIGTWLLDSEALHPL-GMAVKSSXSRGAGGGA 471

Db 165 GLFGTGAGGAGGAGAGGAG-----GSGWLLGNGVGGAGGQSLGATGGAGGNA 217

RESULT 27

A39065

homeotic protein EVX2 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 17-Oct-1997

C;Accession: A39065

R;D'Esposito, M.; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli, E. Genomics 10, 43-50, 1991

A;Title: EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, is

A;Reference number: A39065; MUID:91257849; PMID:1675198

A;Accession: A39065

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-333 <DAE>

C;Genetics:

A;Gene: GDB:EVX2

A;Cross-references: GDB:127528; OMIM:142991

A;Map position: 2q24.3-2q31

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;46-102/Domain: homeobox homology <HGX>

Query Match 4.5%; Score 111; DB 2; Length 333;

Best Local Similarity 23.2%; Pred. No. 0.87;

Matches 74; Conservative 27; Mismatches 116; Indels 102; Gaps 12;

QY 184 SVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLD 243

Db 4 SGSAAGTTTSASGS---GLGSLHGGSGG-----SGGSALGGSGSGADQVRRYRTAFT 53

QY 244 RDDGAK--KVIFY-----VIET-----REPRERLLLTAAH-- 270

Db 54 REQIARLEKFEYRENYVSRPRRCELAAALNLPETTIVKWFQNRMRMKDKRQLAMSWPHEA 113

QY 271 ----LLFVAPHNDSATGE-----PEASSGSGPPSGGALGPRALFASR 308

Db 114 DPSFYTYMTH-AAATGSLPYPFHSHVPLHYYPHVGVTAATAAAAAAASGAAAAASPPFATS 172

QY 309 VRPGQVVVVAERDGRRLLPAAVHSVTLSEEAAGAY-APLTAQGTILINRVLASCYAVI 367

Db 173 IRPLDTFRALSHPHYSRPELLCSFRH-----PGLYQAPAAAAGLNSAASAAAAAAA 224

QY 368 EEHWAHRAFPAP-----FRLAHALLAALAPARTDRGDSGGGDRGGGGG 412

Db 225 AAASSAAAAGAPPSGGGAPCSCLSSQSAASAAAAAALGSRGGGGGGGGGG 283

QY 413 VALTPGAADAPGAGATAG 431

Db 284 -----CGAGAGGG 291

RESULT 28

EDBE75

immediate-early protein IE175 - human herpesvirus 1

C;Species: human herpesvirus 1

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000

C;Accession: A23510

R;McGeoch, D.J.; Dolan, A.; Donald, S.; Brauer, D.H.K. Nucleic Acids Res. 14, 1727-1745, 1986

A;Title: Complete DNA sequence of the short repeat region in the genome of herpes simple

A;Reference number: A23510; MUID:86148504; PMID:3005980

A;Accession: A23510

A;Molecule type: DNA

A;Residues: 1-1298 <MCG>

A;Cross-references: GB:X14112; GB:D00317; GB:D00374; GB:S40593; NID:G1944536; PIDN:CAA3

C;Comment: This protein acts at the transcriptional regulatory level and is required th

C;Genetics:

A;Gene: IE3

A;Map position: short repeat region (IR-s)

C;Superfamily: herpesvirus immediate-early protein IE175

C;Keywords: DNA binding; early protein; transcription regulation

Query Match 4.5%; Score 111; DB 1; Length 1298;

Best Local Similarity 25.8%; Pred. No. 5.1;

Matches 96; Conservative 34; Mismatches 134; Indels 108; Gaps 20;

QY 148 ITTSDDRDRSKY--GMLAR-----LAVEAG-FDWVYVESKAHIHCS----- 184

Db 410 ISGAARNSSSFITGVARAVPHLGYAMAAGRFGWGLAHFAAAAVAMSRRYDRAQKGFLLTS 469

QY 185 -----VKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDR-----VLA 226

Db 470 LERAYAPLLARENAALTGAAGS-PGAGA---DDEGVAAVAAPGERAVPAGYGAAGILA 525

QY 227 ADDQGRLLYS-----DFTFLDRDDGAKK-----VFYVIETREPRERL---- 264

Db 526 A--LGRLSAASPAGGDDPDPAARHADADDDAGRAQAGRVAVECLAACRGILEALAEGF 583

QY 265 ---LLTAAHLLFVAPHNDSATGEPEASSG-SGPPSGGALGPR-----ALFAS 307

Db 584 DGDAAVPLAGARP---ASPPEPGPAGPASPPPHADAPRLRLAWLRELRFVDALVLM 640

QY 308 RVPPGQVVVVAERDGRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYAVI 367

Db 641 RLRGDLRV-----AGGSEAAVAAVRAVSL---VAGALGPALPRDRLPSSAAAAAADLL 691

QY 368 BEHS-----WAHRAFAFRLAHALLAALAPA--RTDRGGDSGGDR--GGGGRRVALTAP 418
Db 692 FDNQSLRPLLAASAP-DAADALAAAAAAPREGKRXKSPGPAPPPGGGPRPKTKK 750
QY 419 GAADAPGAGATA 430
Db 751 SGADAPGSDARA 762

RESULT 29
T35852
probable UDP-N-acetylmuramoyl-L-alanine ligase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: T35852
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21591
A;Accession: T35852
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-462 <SAU>
A;Cross-references: EMBL:AL049727; PIDN:CAB41553.2; GSPDB:GN00070; SCOEDB:SC9B1.07
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC9B1.07
C;Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 4.5%; Score 110; DB 2; Length 462;
Best Local Similarity 26.3%; Pred. No. 1.6;
Matches 47; Conservative 21; Mismatches 71; Indels 40; Gaps 6;

QY 305 FASRVPPQGVVVAERDGRIL--LPAAVHSVTL--SEEAAGAYAPLTAQG-----TI 354
Db 207 FAGKIVPGGTLVIAADHEGARELTRLAGRVRTVYGESEADVRILSVVPOGLKSEVTV 266
QY 355 LINRVLASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGGGRVA 414
Db 267 VLDGAELTFVSVPGRHYAHNA-----VAALAAG-----AA 297
QY 415 LTAPGAADAPGAGATAGIHWSQLLYQ-IGTWLLDSEALHPLGMVKSXSRGAGGGAR 472
Db 298 LGVPAELPALAAAYTGKRRLLQKGEAGVQVVDVSYAHPTMTADLEAMRAAVGDAR 356

RESULT 30
S46458
transcription factor tbx2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S46458
R;Bollog, R.J.; Siegfried, Z.; Cebra-Thomas, J.A.; Garvey, N.; Davison, E.M.; Silver, L.
Nature Genet. 7, 383-389, 1994
A;Title: An ancient family of embryonically expressed mouse genes sharing a conserved pr
A;Reference number: S46458; MUID:95004605; PMID:7920656
A;Accession: S46458
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-701 <BOL>
A;Cross-references: GB:U15566; NID:g558875; PIDN:AAC52697.1; PID:g558876
C;Genetics:
A;Gene: Tbx2
C;Superfamily: mouse transcription factor tbx2; T-box homology
F;104-285/Domain: T-box homology <TBX>

Query Match 4.4%; Score 107.5; DB 1; Length 701;
Best Local Similarity 20.0%; Pred. No. 4.2;
Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;

QY 118 PGVKLRVTEGWDGHHSEESLHYEGRAVDITTSDR-----DRSKYGMRLAR 163
Db 95 PKVTLEAKELWDQ-----FKLGTMTVITKSGRRMFPFKVRVSGLDKKAKYILL-- 144

QY 164 LAVEAGFDWVYVESKAHIHCSVKAENS---VAAKSGGCFPGSATVHLEQGGT----- 212
Db 145 MDIVAADD-----CRYKFHNSRWVWAGKADPEMPKRMVTHPDSPATGEQWMAKP 193
QY 213 -----KLVKDLS-----PGDRVLAADDQGRLLYSDFLTF----- 242
Db 194 VAFHKLKLNNISDKHGFTILNSMHKYQPRPHIVRANILKLPYSTFTYVFPETDFIAV 253
QY 243 -----DRDDGAKKVYFVVIETREPRERLLLTAAHLL--FVAPHND 279
Db 254 TAYQNDKITQLKIDNNPFAKGRDTGNGR-----REKRKQLTLPTRLIYEEHCKPERD 306
QY 280 SATGEPEASS-----GSGPPSGGALGPRALFASRVVRPGQVVV-----AERDGDRLRLP 329
Db 307 GA--ESDASSCDPPPARPPSPSAAPSPLRLHRAAEKPGAADSDPEPERTGEER--- 361
QY 330 AAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYAVIEEHSWAHRAFAFRLAHALLA- 388
Db 362 -----SAAPLCRSPS-----RDASPARLTERPERSR 386
QY 389 -ALAPARTDRGGDSGGD-----RGGGGRRVALTAP----- 418
Db 387 ERSRPERCSKEPTEGGGDPFSLRLEKERPEARKEDEGRKDVGEKGPSLAPLVVQTDS 446
QY 419 -----GAADAPGAGATAGIHWY-----SLLYQIGTWLLDSEALHPLGM-----A 458
Db 447 ASPLGAGHLPLGLAFSSHLHGQQFFGLGACQPLFLHPGQFAMGPGAFSAMGHLASVA 506
QY 459 VKSSXSRGAGGGGAREG 474
Db 507 GGSSSGGAGPGTAAG 522

RESULT 31
EDBE11
immediate-early protein IE110 - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 17-Mar-2000
C;Accession: A29152
R;Perry, L.J.; Rixon, F.J.; Everett, R.D.; Frame, M.C.; McGeoch, D.J.
J. Gen. Virol. 67, 2365-2380, 1986
A;Title: Characterization of the IE110 gene of herpes simplex virus type 1.
A;Reference number: A29152; MUID:87059760; PMID:3023529
A;Accession: A29152
A;Molecule type: DNA
A;Residues: 1-775 <PER>
A;Cross-references: GB:X04614; NID:g59832; PIDN:CAA28285.1; PID:g59833
C;Genetics:
A;Introns: 19/3; 242/1
C;Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;112-162/Domain: RING finger homology <RNG>
F;116-156/Region: zinc finger C3HC4 motif

Query Match 4.3%; Score 107; DB 1; Length 775;
Best Local Similarity 26.7%; Pred. No. 5.2;
Matches 68; Conservative 18; Mismatches 89; Indels 80; Gaps 12;

QY 275 APHNDSATGEPEASSGSGPPSGGALG---PRALFASRV-----PGQVVV---VAER 321
Db 371 SPHRPPAAPMPGSAAPRPGPPASAAAGPARPRAAVAPCVRAPPPGPGPRAPAGAEPAAR 430
QY 322 DGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYAVIEEHSWAHRAFAFPR 381
Db 431 PADARRVPQS-HS-SLAQAANQEQLCRARATV----ARGSGGPGVEGGHGPSRGAAPSG 484
QY 382 LAHALLAA-----LAPARTDRG-----GDSGGGDRG 407
Db 485 AAPLPSAASVEQEAAVPRKRRSGSQENPSPQSTRPPLAPAGAKAATHPPSDSGPGGRG 544
QY 408 GGGRRVALTAPGAADAPGAGATAGIHWSQLLYQIGTWLLDSEALHPLGM-----AVKS 461

Db 545 QGGPGTPLTS-SAASASSSSASS-----SSAPTPAGAASSAACAASS 585

QY 462 SXSRGAGG--GAREG 474

Db 586 SASASSGGAVALGG 600

RESULT 32

E70554

hypothetical protein Rv1148c - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C;Accession: E70554

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: E70554

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-482 <COL>

A;Cross-references: GB:Z95584; GB:AL123456; NID:93261774; PIDN:CAB09036.1; PID:92117186

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv1148c

C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1945

Query Match 4.3%; Score 106.5; DB 2; Length 482;

Best Local Similarity 22.0%; Pred. No. 3.1;

Matches 87; Conservative 40; Mismatches 151; Indels 117; Gaps 16;

QY 49 PNVAKETLGASRGVEGKISRNSR-----PKELTPNYPNDIIFKDEBENTGADRLMTQRCK 103

Db 137 PLPAQLTATAAQRGKIGREHIKEIQAFFKELSAV--DLGIREAAEAQLAELATSRRP 194

QY 104 DKLNALAISVMNQVGKLRVTEGWDEGDHSEESLHYEGRVADITTSDDRRS-KYGMLA 162

Db 195 DHLHGLATQLMD-----W-----LHPDG-----NPSDQERARKRGITM 227

QY 163 RLAVEAGFDWVYVESKAHHCVKAENSVAAKSGGCFPGSATVHLEQGTKLVKDLSPGD 222

Db 228 GKQEFDGMSRISGLLTPPELRATIEAVLAKLAAPGACNPDDQ-----TPLVDDTTPDAD 279

QY 223 RVLA-ADDQGRLLYSDFLTFLDRDDGAKKVFVVIETREPRERLLLTAAHL-----LFVAP 276

Db 280 AVRDRTRSQAQRNHDAFLAAL-----RGLLASGELGQHKGLPVTI 319

QY 277 HNDSATGEPEASSGSGPPSGGA-----DRRLPAAVHSHVTLSEBAAGAYAPLTAQGTILINRVLASCYA 365

Db 320 VVSTTIKELEAATGKGTGGSRVPMSDLIRWASHANHYLALFDGAKPLALYHTKRLASP 379

QY 312 GQRVVVVAERDG-----DRRLPAAVHSHVTLSEBAAGAYAPLTAQGTILINRVLASCYA 365

Db 380 AQRIMLYAKDRGCSRPGCDAPAYHSEVHVHT-----PWTTHRTDINDLTILACGP 429

QY 366 --VIEEHSWAHRAFAFAPFLAHALLAALAPARTDRG 398

Db 430 DNRLVEKGWKTR-----KNAHGDTWELPPPHLDHG 459

RESULT 33

JC7583

basic helix-loop-helix protein, DEC2 - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7583

R;Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E.

Biochem. Biophys. Res. Commun. 280, 164-171, 2001

A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-loop-helix

A;Reference number: JC7583; MUID:21092582; PMID:11162494

A;Accession: JC7583

A;Molecule type: mRNA

A;Residues: 1-482 <FUG>

A;Cross-references: DDBJ:AB044088

C;Comment: This protein, a novel member of the DEC subfamily of basic helix-loop-helix

C;Genetics:

A;Gene: dec2

A;Map position: 12p11.23-p12.1

C;Keywords: transcription factor

F;1-173/Region: highly conserved #status predicted

F;130-173/Domain: Orange #status predicted <ORA>

F;286-411/Region: alanine and glycine-rich #status predicted

Query Match 4.3%; Score 106; DB 2; Length 482;

Best Local Similarity 24.7%; Pred. No. 3.4;

Matches 77; Conservative 21; Mismatches 94; Indels 120; Gaps 16;

QY 204 TVHLEQGTKLVKDLSPGDRVLAADDQGRLL--LYSDFLTFLDRDDGAKKVFYVI---ETR 258

Db 100 TALTEQQHQKIIA-LQNGERSLKSPIQSDLDLDAFHSGFQTC-----AKEVLQYLSRFESW 152

QY 259 EPRE-RLLLTAHLLFVA----PHNDSATGEPEASSGSGPPS--GGALGPRALFASRVRP 311

Db 153 TPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAP-----CLERA 207

QY 312 GQRV---YVV-----AERD-----GDRRLP-----AAVHSVTLSE 339

Db 208 GQKLEPLAYCVPVIQRTQPSAEAAENDTDTDSGYGGEAEARPDREKXGKAGASRVTIKQ 267

QY 340 EAAGAYAPLTAQGTILINRVLASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGG 399

Db 268 EPPGEDSP-----APKRM-----KLDSEALHPLGMVAV 459

QY 400 DSGGDRGGGGRVALTPAGAADAPGAGATAGIHWYSQLLYQIGTWLDDSEALHPLGMVAV 459

Db 288 GSGGGPGGG-----AAAAAALLGPDPAATAAL-----LRPDAALL 323

QY 460 KSSXSRGAGGGA 471

Db 324 SSLVAFGGGGGA 335

RESULT 34

T09084

phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)

C;Species: Chlamydomonas reinhardtii

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Accession: T09084

R;Molendijk, A.J.; Irvine, R.F.

Plant Mol. Biol. 37, 53-66, 1998

A;Title: Inositol signalling in Chlamydomonas: Characterization of a phosphatidylinosi

A;Reference number: Z16411; MUID:98281574; PMID:9620264

A;Accession: T09084

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-490 <MOL>

A;Cross-references: EMBL:U97663; NID:92109290; PIDN:AAC50018.1; PID:92109291

A;Experimental source: strain cw-15

C;Genetics:

A;Introns: 265/3; 331/3; 370/3; 455/1; 481/3

Query Match 4.3%; Score 105.5; DB 2; Length 490;

Best Local Similarity 25.1%; Pred. No. 3.7;

Matches 76; Conservative 23; Mismatches 123; Indels 81; Gaps 15;

QY 191 VAAKSGGCFPGSATVHLEQGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFL---DRDD 246

Db 234 LAAGGG---GGG-----SGSGSTAR-----WDEWLTFCVKYRDLPP 271

QY 247 GAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGGALGPRALFA 306

Db 272 DAQLVLLVEAAEGRREALVCGSSVTPLFSKRGRLKTPQRLAVWEGAP-----PCTQFP 325

Db 218 VARFIQDDLKQSPYGIIRLIQSGSHIIVPKLYEGEHAYILQNEDDRRIIVEIPAIPYLDRTFMIG 277
QY 243 --DRD---DGAK-----KVFYVIETREPRERLLTAAHLLF-----VAPHNDSATGEPEA 287
Db 278 TTDRYQGDPAKVAISEETAYLLQVVNAHFQQLAAADILHSFAGVRPLCDDSEDEPSA 337
QY 288 -----SSGSGPPS-----GGALGP-RALFASRVPRGQRYVVVAERDGRRLLPAAV 332
Db 338 ITRDYTLSLSAGNGEPPLLSVFGGKLTTRYKLAESALTQLQPPFA-----NLGPAWT 389
QY 333 HSVTLSEEAAGAYAPLTA-----QGTILINRVLASCYAVIEEHSWAHRAFAFAPRLAH---- 384
Db 390 -----AKAPLPGGEQMQSVEALTEQLANRYA-----WLDRELAPALGAHYGTR 432
QY 385 --ALLAALAPARTDRGDSGGDRGGG 410
Db 433 VMRLLDGV-----NGEADLGEHLGG 453

RESULT 40

S25077
monensin polyketide beta-ketoacyl synthase (EC 2.3.1.-) chain 2 - Streptomyces cinnamonensis
C:Species: Streptomyces cinnamonensis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S25077; S18168
R:Arrowsmith, T.J.; Malpartida, F.; Sherman, D.H.; Birch, A.; Hopwood, D.A.; Robinson, J.
Mol. Gen. Genet. 234, 254-264, 1992
A:Title: Characterisation of actI-homologous DNA encoding polyketide synthase genes from
A:Reference number: S25076; MUID:92374994; PMID:1508151
A:Accession: S25077
A:Molecule type: DNA
A:Residues: 1-402 <ARR>
A:Cross-references: EMBL:Z11511; NID:946799; PIDN:CAA7597.1; PID:946801
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-protein]
C:Keywords: acyltransferase
F:22-398/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 4.2%; Score 104; DB 1; Length 402;
Best Local Similarity 24.1%; Pred. No. 3.7;
Matches 95; Conservative 33; Mismatches 140; Indels 126; Gaps 21;
QY 140 HYEGRVADITTSDDRSKYGMLARLAVEAGFDWVYVESKAHHCVSVAENSV--AAKSGG 197
Db 60 HLPGRVLPQT----DR-----VTRLSLAAA-DWALADAGVEVAADFPLDMGVVTASHAGG 109
QY 198 CFPGSATVHLEOGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLDRDDGAKKVFY---- 253
Db 110 -----FEFGQDELQKLLGQGPVLSA-----YQSFAPFYAVNSGQISIRHGMKG 153
QY 254 -----VIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSPGGALGPR 302
Db 154 PSGVVVSDQAGLDALAAQARRLVKGTPLIV-----CGAVEPRAPGAGSPSPAGG-- 205
QY 303 ALFASRVPRGQRYVVVAERDGRRLLPAAVHSHVTLSEEAAGAYAPLTAQGTILINRVLAS 362
Db 206 ---MSDSDEPNAYLPFDRDG-RGYVPGGGRGVVPFLERAEE-AP--ARGA----- 249
QY 363 CYAVIEEHSWAHRAFAFPF-----RLAHALLAALAPARTDRG-----GDSGG--GDRGG 408
Db 250 --EVYGEAGPLARLPAPHSGRGSTRAHAIRTAALDDAGTAPGDIRRVFADGGGRYPNDRAE 307
QY 409 -----GGGRVALTAP-----GAADAPGAGA---TAGI-----HWY 435
Db 308 ABAISEVFGPRVFTCPRTMTGRHLHSGAAPLDVACALLAMRAGVTPPTVHIDPCPEYDL 367
QY 436 SQLLYQIGTWLDDSEALHPLGMVAKSSXSRGAGG 469
Db 368 DLVLYQV-----RPAALRTALGGARGHGG 391

RESULT 41

A40253
acidic nuclear protein SPT5 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YM9571.08; protein YML010W
C:Species: Saccharomyces cerevisiae
C:Date: 06-Dec-1991 #sequence_revision 06-Dec-1991 #text_change 29-Oct-1999
C:Accession: A40253; S55109
R:Swanson, M.S.; Malone, E.A.; Winston, F.
Mol. Cell. Biol. 11, 3009-3019, 1991
A:Title: SPT5, an essential gene important for normal transcription in Saccharomyces cerevisiae
A:Reference number: A40253; MUID:91246167; PMID:1840633
A:Accession: A40253
A:Molecule type: DNA
A:Residues: 1-1063 <SWA>
A:Cross-references: GB:M62882; NID:g172679; PIDN:AAA35085.1; PID:g172680
R:Gentles, S.; Bowman, S.
Submitted to the EMBL Data Library, June 1995
A:Reference number: S55109
A:Accession: S55109
A:Molecule type: DNA
A:Residues: 1-1063 <GEN>
A:Cross-references: EMBL:Z49810; NID:g854472; PIDN:CAA89942.1; PID:g854480; MIPS:YML010W
A:Experimental source: strain AB972
C:Genetics:

A:Gene: SGD:SPT5
A:Cross-references: SGD:S0004470; MIPS:YML010W
A:Map position: 13L
C:Keywords: nucleus; tandem repeat
F:148-216/Region: aspartic acid/glutamic acid-rich
F:931-1063/Region: 6-residue repeats

Query Match 4.2%; Score 104; DB 2; Length 1063;
Best Local Similarity 21.6%; Pred. No. 13;
Matches 119; Conservative 61; Mismatches 203; Indels 168; Gaps 29;

QY 45 KQFIPNVAEKTLCASGRYEG-----KISRNSERFKELTPNYPD--IIFKDEENTGADRL 97
Db 496 KNIQPTVEE--LARFGSKEGAVDLTSVSQSIKKAQAQAKVTFQPGDRIEVLNGEQRGSKGI 553
QY 98 MTQRCKD-----KLNALA-----ISVMNQ--WPGVKLRVTEGWDEDEGHHSSESL----- 139
Db 554 VTRTTKDIATIKLNGFTTLPLEFPILTSLRKIFEPGDHVTVING-----EHQGDAGLVLMVEQ 609
QY 140 -----HYEGRVADITTSDDRSKYGMLARLAVEAGFDWVYVESKAHHCVSVAENSV- 191
Db 610 QGVTFMSTQTSREVTITANNLSKS-IDTTATSEYALHDIIVELSAK-NVACIIQAGHDIF 667
QY 192 -----AAKSGCFPGSATVHLEOGGTKLVKDLSPGDRVLAADD-----QGRLLYS 237
Db 668 KVIDETKGVSTITKGSILSKINTARARVSSVDANGNEIKIGDTIVEKVSRRREGQVLYIQ 727
QY 238 FLTFLDRDDGAKKVFYVIETREPRERLLTAAHLLFVAPHN-----DSAT 282
Db 728 -----TQQIFV-----SKKIVENAGVFVVPNSVNEAVASKDNMLSNKMDLSK 770
QY 283 GEPEASSGSGPPS-----CG-----ALGPRALFASRVPRGQRYVVVAERDGRRL 328
Db 771 MNPEIISKMGFPSSKTFQPIQSRGGREVALGKTVIRISAGYKGO-LGIVKDVNGDKATV 829
QY 329 PAAVHS-----VTLSEEAAGAYAPLTAQGTI---LINRVLASCYAVIEEHSWAHRAFAF 381
Db 830 --ELHSKNKHITIDKHKLTYNREGGEGITYDELVNR-----RGRVPQARMGSPSYVSAPRN 883
QY 382 LAHALLAALA-----PARTDRGDSGGG-----DRGGGG 411
Db 884 MATGGIAAGAAATSSGLSGGMTPGWSSFDGKTPAVNAHGGSGGGGVSSWGGA 943
QY 412 RVALTPGAADAPGAGATAGIHWYSQLLYQIGTWLDDSEALHPLGMVAV---KSS---XS 464
Db 944 NGGASAWGGA---GGGASA---WGGQGTGATSTW-----GGASAWGNKSSWG 987
QY 465 RGAGGGAREGA 475
Db 988 TWASGGESNGA 998

RESULT 42

T30342
protein HMWP1 - *Yersinia enterocolitica*
C;Species: *Yersinia enterocolitica*
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 01-Dec-2000
C;Accession: T30342
R;PELLUDAT, C.; RAKIN, A.; JACOBI, C.; SCHUBERT, S.; HEESERMANN, J.
J. Bacteriol. 180, 538-546, 1998
A;Title: The yersiniabactin biosynthetic gene cluster of *Yersinia enterocolitica*: organization and function
A;Reference number: Z20833; MUID:98117033; PMID:9457855
A;Accession: T30342
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3161 <PEL>
A;Cross-references: EMBL:Y12527; NID:el228641; PID:el228642; PIDN:CAA73127.1

RESULT 43

S33121 homeotic protein CDP - dog (fragment)
 N;Alternate names: CCAAT displacement protein; homeotic protein Clox
 C;Species: Canis lupus familiaris (dog)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
 C;Accession: S33121
 R;Andres. V.; Nadal-Ginard, B.; Mahdavi, V.

Development 116, 321-334, 1992
A;Title: Clox, a mammalian homeobox gene related to Drosophila cut, encodes DNA-binding
A;Reference number: S33121; MUID:93161940; PMID:1363085

RESULT 44

E70661
 probable PE protein - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C;Accession: E70661
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: E70661
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-413 <COL>
 A;Cross-references: GB:Z83860; GB:AL123456; NID:g3261681; PIDN:CAB06157.1; PID:g1781247
 A;Experimental source: strain H37RV

C;ACCESSION: S33121
R;Andres, V.: Nadal-Ginard, B.; Mahdavi, V.

Db 80 LQEGAAAYAMAEANAL-----PLOKAQGVVSELAQDRT-- 113

QY 398 GGDSSGGDRGGGRVALTAPGAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHP--- 454

Db 114 GGTGTGQSRGAGG-----FGGVGQAGGKGWDGPGTGNQVGEQHGAGQLGSTDGNPGVA 167

QY 455 ---LGMVVKSSXSRGAGGGA 471

Db 168 GAAHSGSVSASHGSGATGAA 187

RESULT 45

F70573

hypothetical protein Rv0341 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C;Accession: F70573

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: F70573

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-479 <COL>

A;Cross-references: GB:Z95324; GB:AL123456; NID:G3261760; PIDN:CAB08573.1; PID:G2094820

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv0341

C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match 4.2%; Score 102.5; DB 2; Length 479;

Best Local Similarity 24.6%; Pred. No. 6.1;

Matches 77; Conservative 30; Mismatches 115; Indels 91; Gaps 13;

QY 237 DFLTFLDRDDGAKKVFYVIETREPRERLLTLTAHLLFVAPHNDSATGE---PRASSGSGP 293

Db 6 DYILSLRSEDAARSFVAAPGR-----AMTSAGLIDIAFHQISSVAANVVPGLNLGAGD 59

QY 294 PSGGALGPRALFASRVPRGQVVVVAERDGRRLLPAAVHVSRTLSEEAAGAYAPLTA--- 350

Db 60 PMSGL---RQAVAAHGHFAQDVANVCFA-GD---AGAGVASVITTDVGAGLASGLGAGFL 112

QY 351 -QGTI-----LINRVLASCYAVIEEHSWAHRAFPRL-----AHALLAAL 390

Db 113 GQGLALAASSGGFGGQVGLAAQVGLGFTAVIEAEVGA-QVGAGLGIGTGLGAQAGMGFG 171

QY 391 APARTDRGDSGG-----GDRGGGGRVALTAPGAADAPGAGATAGIHWS 436

Db 172 GGVGLGLGGQAGGVIGGSAAGAIGAGVGGRLGGNGQIGVAGQCAV---GAGVGAGVGGQA 228

QY 437 QLLYQIG-----TWLLDSE---ALHPLGMVAVKSS 462

Db 229 GIASQIGVSAGGGLGGVGNVSLTGVSSNAVLASNASQAGLIASEGAALNGAAMPHLSG 288

QY 463 XSRGAGGGAREGA 475

Db 289 PLAGVGVGGQAGA 301

RESULT 46

T27975

hypothetical protein ZK678.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T27975

R;Kershaw, J.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20449

A;Accession: T27975

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-481 <WIL>

A;Cross-references: EMBL:Z79605; PIDN:CAB01902.1; GSPDB:GN00028; CESP:ZK678.5

A;Experimental source: clone ZK678

C;Genetics:

A;Gene: CESP:ZK678.5

A;Map position: X

A;Introns: 33/3; 99/3; 131/2; 211/1; 324/3; 342/1; 381/3; 436/3

Query Match 4.2%; Score 102.5; DB 2; Length 481;

Best Local Similarity 19.0%; Pred. No. 6.1;

Matches 39; Conservative 25; Mismatches 36; Indels 105; Gaps 5;

QY 188 ENSVAAKSGG-----CFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGR 232

Db 321 QNPVPAAPAGYAPMGFAPSGQLYYCFFPGDAMVNVYNGGFKRMDELAVGDWVQA----- 374

QY 233 LLYSDFLTFLDRDDGAKKVFYVIETREPRERLLTLTAHLLFVAPHNDSATGEPEASSGSG 292

Db 375 -----LDKNGSQSQSMY----- 386

QY 293 PPSGALGPRALFASRVPRGQVVVVAERDGRRLLPAAVHVSRTLSEEAAGAYAPLTAQG 352

Db 387 -----QRVKVL-----DINIV-----QKTGIYSPMTSRG 410

QY 353 TILINRVLASCYAVIEEHSWAHRAF 377

Db 411 HLLVDRIHASCHSETDNYSLQNTFF 435

RESULT 47

B75625

hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C;Accession: B75625

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: B75625

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1145 <WHI>

A;Cross-references: GB:AE001826; NID:G6460827; PIDN:AAF12641.1; PID:G6460937; TIGR:DRB00

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRB0065

A;Map position: megaplasmid

A;Genome: plasmid

A;Note: plasmid MP1

Query Match 4.1%; Score 102; DB 2; Length 1145;

Best Local Similarity 19.9%; Pred. No. 21;

Matches 88; Conservative 51; Mismatches 167; Indels 136; Gaps 18;

QY 90 ENTGADRLMTQRCCKLNLALAISVMNQWPGVKLRVTEGWEDCHHSESLHYEGRAVDIT 149

Db 644 QSNGAAHL-----RNDLQALATSMDSLESIVTMPAGNPDSDA-----LTGQPVQVL 690

QY 150 TSDRDRSKY--GMLARLAVEAGFDVYVESKAHHCISVKAENSVAAKSGGCGPFSATVHL 207

Db 691 TDNGDSVYVYGDGKIADLVAPAQDWQKFRPAETVIVGALPAQTCTVSNL-SVTPDNST--L 747

QY 208 EQGGTKLVKDL-----SPGDRVLAADDQGRLLYSDFLTFLDRDDGAKKVF 252

Db 748 PVGGTQTFKAIYTTSPNCANVSVSSSDPSKLTVDERG----- 786

QY 253 YVIETREPRERLLTLTAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALFASRVPRG 312

Db 787 --VARBAAGTVTLTAT---VTP-----CSGAPVSASTGVTVSAPVTSLPN 827

QY 313 QRVYVVAERDGDRLLPAA-----VHSTVLSEEAAGAYAPLTAQGTI--- 354

Db 828 VAVYRVG--DGSAKLTSAAFPVVDIINPNDGSLVRTLSLPTSTSGSNRPLLASGTASSE 885

QY 355 -LINRVLASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGG-----DSGGG 404

Db 886 GMLTRSADAHYLVLTGYA-ASVGLANVKASDSATTPRVICRLDSAGTVDTTTLPLDAYSG 944

QY 405 DR-----GGGGRRVALTAPGAADAPGAGATAGIHWYSQLLYQIGTWLLDSE 450

Db 945 DNIRSAASTDGRSFYVTGNSGVRLYALGASSGLSISSAA-----SNLRQLGIF---GD 995

QY 451 ALHPLGMVAVKSSXSRGAGGGAR 472

Db 996 QLY-----VSSGSGNGTK 1008

RESULT 48

T00373

hypothetical protein KIAA0649 - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C;Accession: T00373

R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.

DNA Res. 5, 169-176, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete

A;Reference number: Z14142; MUID:98403880; PMID:9734811

A;Accession: T00373

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1209 <ISH>

A;Cross-references: EMBL:AB014549; NID:G3327111; PIDN:BAA31624.1; PID:G3327112

A;Experimental source: brain

C;Genetics:

A;Note: KIAA0649

Query Match 4.1%; Score 102; DB 2; Length 1209;

Best Local Similarity 20.9%; Pred. No. 22;

Matches 106; Conservative 52; Mismatches 220; Indels 128; Gaps 20;

QY 14 SLLVCSGLACGPG-----RGFGKRRHPKKLTPLAYKQFIPNVAEKTILGASGRYEGKISR 68

Db 644 SEALGGEGTARGPGDTRMSQGGKTDEARRLD-----EK-----ES 679

QY 69 NSERFKELTPNPNPDIIFKDEENTGADRLMTQRCKD-----KLNALAI SVMNQWPG 119

Db 680 SEDKSSSLDSDELDTAIKD--LLRSKRKLKKECREPRAACRKKVFSTAQTHFEQLG 737

QY 120 VKLRVTEGWEDEGHSEESLHYEGRAVDITTSDDRR-----SKYGMRLARLAVEAGF 170

Db 738 LR-----RDWKORGPFPVLKSC-----LSKSKRDSGEGPGKKPPSVFGSTAERMROEG- 784

QY 171 DMVYYESKAHIIHCSVKAENSVAAKSGGCGFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQ 230

Db 785 ---AASQDAALAFVRPASPASASEGNPFPRSE-----QGPAPSPGSLSDSSSVSDSDS 836

QY 231 GRLLYSDFLTFLDRDDGAKKVFYVIETREPRERLLTLTA-----AHLFFVAPH 277

Db 837 IELEIRKFLA-----EKAKESVSSSEVQAEPTALGTGGPARPEVLCRKEPAPPPGVCTR 891

QY 278 NDSATGEPEASSG-SGPPSGGALGPRALFASRVPRGQRYVVAERDGRLLPAAVHSV 336

Db 892 SQRARGVPHLAEGRLRGTESAGAQTAGLFSQ-----GGKGLPAAAPARGD-----PVPPRSTS 943

QY 337 LSEEAAGAYAPLTAQGTILINRVLASCYAVIEHSHWAHRAFAF-----FRLAHALLAAL 390

Db 944 GGVSAGK-----LSVSRNRNVVHKDQSPRGAEPAPKSAFQQLPSC 983

QY 391 APARTDRGDSGGDRGGGRVALTAPGAADAPGAGATAGIHWYSQLLYQI---GTWLL 447

Db 984 ATAGTEAGGARGTTFHMGSGSPSFLTPSPGAERDAGAQAADRTPPW-SDFAHQSRLPSPWVL 1042

QY 448 DSEALHPLGM-AVKSSXSRGAGGGAR 472

Db 1043 RSEGRDAVWRGGVGSERDKGSEGPAP 1068

RESULT 49

B84339

hypothetical protein Vng1880c [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: B84339

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: B84339

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-506 <STO>

A;Cross-references: GB:AE004437; NID:G10581323; PIDN:AAG20078.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG1880C

Query Match 4.1%; Score 101.5; DB 2; Length 506;

Best Local Similarity 22.6%; Pred. No. 7.8;

Matches 82; Conservative 39; Mismatches 127; Indels 115; Gaps 19;

QY 131 DGHSEESLHYEGRAVDITT-----SDRDRSKYGMRLARLAVEAGFDWVYYESKAHIHC 183

Db 25 DPAHSAVAIR-DGRIVGLSNDYDAAFRADTGTREVDLGGRVVPGFVD-----AHTHL 76

QY 184 SVKAENSVAAK-SGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLL----- 234

Db 77 AVLKGHGVHADLRGADSPAATARLAERAE-----TDAGWVLGFGYDDSQ 122

QY 235 YSDFLTFLDRDDGAKKVFYVIETREP---RERLLLTAAHLLFVAPHNDSATGEPEASSGS 291

Db 123 WSAALSTADLD-----AVSEARPVAAIREDMHTATVNGVALAEHGDEN---PAADV 171

QY 292 GPPSGGALGPRALFASRVPRGQRYVVAERD--GDRRLLP-----AVHSVTLS 338

Db 172 ---EDGRIVEDAV-----EAVYDATDPLAGTRPLIEAAQREANERGVTAVHEMVRD 220

QY 339 EEAAGAYAPLTAQGTILINRVLASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRG 398

Db 221 SHAPRVYRELDAAGELSVR-----VRLNFWAD-----HLDAVLETLV---TNHG 262

QY 399 GD--SGGGDR---GGGGRRVALTAPGAADAPGAGATAGIHWYSQLLYQIGTWLLDSEAL 452

Db 263 GGMVTVGGIKTYTDGSLGGRGRTAKLSEPYADAPG-----ETGQWVVDPSAL 307

QY 453 HPL 455

Db 308 AAL 310

RESULT 50

C70584

probable serine-threonine protein kinase - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jun-2002

C;Accession: C70584

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

Search completed: March 29, 2004, 18:34:07
Job time : 28 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 18:24:49 ; Search time 17 Seconds
(without alignments)
1454.901 Million cell updates/sec

Title: US-09-883-848A-15
Perfect score: 2469
Sequence: 1 MILLARCLLLVSSLLVCS.....GMAVKSSXSRGAGGGAREGA 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|--------|---------------|--------|--------------|---------------------|
| 1 | 2407 | 97.5 | 462 | 1 SHH_HUMAN | Q15465 homo sapien |
| 2 | 2068 | 83.8 | 437 | 1 SHH_MOUSE | Q62226 mus musculus |
| 3 | 2060 | 83.4 | 437 | 1 SHH_RAT | Q63673 rattus norv |
| 4 | 1807 | 73.2 | 425 | 1 SHH_CHICK | Q91035 gallus gall |
| 5 | 1539.5 | 62.4 | 432 | 1 SHH_CYNPY | Q90385 cynops pyrr |
| 6 | 1506 | 61.0 | 418 | 1 SHH_BRARE | Q92008 brachydanio |
| 7 | 1498 | 60.7 | 444 | 1 SHH_XENLA | Q92000 xenopus lae |
| 8 | 1432 | 58.0 | 416 | 1 TWHH_BRARE | Q90419 brachydanio |
| 9 | 1282.5 | 51.9 | 408 | 1 IHH_CHICK | Q98938 gallus gall |
| 10 | 1271 | 51.5 | 411 | 1 IHH_HUMAN | Q14623 homo sapien |
| 11 | 1262 | 51.1 | 411 | 1 IHH_MOUSE | Q97812 mus musculus |
| 12 | 1248 | 50.5 | 409 | 1 IHH_XENLA | Q91612 xenopus lae |
| 13 | 1213 | 49.1 | 412 | 1 IHH_BRARE | Q98862 brachydanio |
| 14 | 1183 | 47.9 | 396 | 1 DHH_MOUSE | Q61488 mus musculus |
| 15 | 1177 | 47.7 | 396 | 1 DHH_HUMAN | Q43323 homo sapien |
| 16 | 1079.5 | 43.7 | 396 | 1 DHH_XENLA | Q91610 xenopus lae |
| 17 | 1077.5 | 43.6 | 398 | 1 DHH2_XENLA | Q91611 xenopus lae |
| 18 | 890 | 36.0 | 421 | 1 HH_DROME | Q02936 drosophila |
| 19 | 854 | 34.6 | 422 | 1 HH_DROHY | P56674 drosophila |
| 20 | 602 | 24.4 | 121 | 1 SHH_RASEL | P79858 rasbora ele |
| 21 | 599 | 24.3 | 121 | 1 SHH_CARAU | P79691 carassius a |
| 22 | 599 | 24.3 | 121 | 1 SHH_PUNTE | P79850 punctius tet |
| 23 | 598 | 24.2 | 121 | 1 SHH_RASHE | P79864 rasbora het |
| 24 | 598 | 24.2 | 121 | 1 SHH_RASPA | P79869 rasbora pav |
| 25 | 597 | 24.2 | 121 | 1 SHH_TANAL | P79915 tanichthys |
| 26 | 595 | 24.1 | 121 | 1 SHH_AMECH | P79682 amblypharyn |
| 27 | 594 | 24.1 | 121 | 1 SHH_DANAA | O13235 danio aff. |
| 28 | 594 | 24.1 | 121 | 1 SHH_DANAE | O13234 danio aequi |
| 29 | 594 | 24.1 | 121 | 1 SHH_DANAT | O13238 danio aff. |
| 30 | 594 | 24.1 | 121 | 1 SHH_DANFR | O13245 danio frank |
| 31 | 594 | 24.1 | 121 | 1 SHH_DANKE | P79709 danio kerri |
| 32 | 594 | 24.1 | 121 | 1 SHH_DANPU | P79717 danio pulch |
| 33 | 594 | 24.1 | 121 | 1 SHH_DEVDE | O13241 devario dev |

| | | | | | |
|-----|-------|------|------|--------------|---------------------|
| 34 | 594 | 24.1 | 121 | 1 SHH_DEVMA | O13247 devario mal |
| 35 | 594 | 24.1 | 121 | 1 SHH_DEVPA | O13250 devario pat |
| 36 | 590 | 23.9 | 121 | 1 SHH_PUNCO | P79838 punctius con |
| 37 | 396 | 16.0 | 88 | 1 DHH_BRARE | P79729 brachydanio |
| 38 | 293 | 11.9 | 58 | 1 IHH_CARAU | P79693 carassius a |
| 39 | 293 | 11.9 | 58 | 1 IHH_DANAT | O13240 danio aff. |
| 40 | 293 | 11.9 | 58 | 1 IHH_DANKE | P79711 danio kerri |
| 41 | 293 | 11.9 | 58 | 1 IHH_DANPU | P79719 danio pulch |
| 42 | 293 | 11.9 | 58 | 1 IHH_DEVDE | O13243 devario dev |
| 43 | 293 | 11.9 | 58 | 1 IHH_PUNTE | P79852 punctius tet |
| 44 | 293 | 11.9 | 58 | 1 IHH_RASEL | P79860 rasbora ele |
| 45 | 289 | 11.7 | 58 | 1 SHH_PSEPR | P79839 pseudorasbo |
| 46 | 288 | 11.7 | 58 | 1 DHH_DANKE | P79712 danio kerri |
| 47 | 288 | 11.7 | 58 | 1 IHH_DEVMA | O13215 devario mal |
| 48 | 288 | 11.7 | 58 | 1 IHH_RASHE | P79866 rasbora het |
| 49 | 287 | 11.6 | 58 | 1 IHH_DEVPA | O13220 devario pat |
| 50 | 287 | 11.6 | 58 | 1 IHH_RASPA | P79871 rasbora pav |
| 51 | 280 | 11.3 | 58 | 1 DHH_PUNTE | P79853 punctius tet |
| 52 | 277 | 11.2 | 53 | 1 TWHH_PSEPR | O13226 pseudorasbo |
| 53 | 275 | 11.1 | 53 | 1 TWHH_CARAU | P79696 carassius a |
| 54 | 275 | 11.1 | 53 | 1 TWHH_DANKE | P79715 danio kerri |
| 55 | 275 | 11.1 | 53 | 1 TWHH_DEVPA | O13253 devario pat |
| 56 | 275 | 11.1 | 53 | 1 TWHH_PUNTE | P79855 punctius tet |
| 57 | 270 | 10.9 | 53 | 1 TWHH_DANFR | O13212 danio frank |
| 58 | 163.5 | 6.6 | 557 | 1 WRT4_CAEEL | Q94129 caenorhabdi |
| 59 | 135.5 | 5.5 | 485 | 1 WRT1_CAEEL | Q94128 caenorhabdi |
| 60 | 129 | 5.2 | 1147 | 1 MYSB_ACACA | P19706 acanthamoeb |
| 61 | 128 | 5.2 | 550 | 1 WRT2_CAEEL | Q94130 caenorhabdi |
| 62 | 125.5 | 5.1 | 476 | 1 EVX2_HUMAN | Q03828 homo sapien |
| 63 | 118.5 | 4.8 | 702 | 1 TEX2_HUMAN | O13207 homo sapien |
| 64 | 115.5 | 4.7 | 940 | 1 GLND_CAUCR | Q9ac53 caulobacter |
| 65 | 111 | 4.5 | 1298 | 1 ICP4_HSV11 | P08392 herpes simp |
| 66 | 110 | 4.5 | 462 | 1 MURC_STRCO | Q9x827 streptomyce |
| 67 | 107.5 | 4.4 | 701 | 1 TEX2_MOUSE | Q60707 mus musculu |
| 68 | 107 | 4.3 | 775 | 1 ICP0_HSV11 | P08393 herpes simp |
| 69 | 106.5 | 4.3 | 454 | 1 YB48_MYCTU | O06548 mycobacteri |
| 70 | 106 | 4.3 | 482 | 1 BHB3_HUMAN | Q9c0j9 homo sapien |
| 71 | 106 | 4.3 | 1067 | 1 BAB2_DROME | Q9w0k4 drosophila |
| 72 | 105.5 | 4.3 | 494 | 1 AMYR_DROKI | O77013 drosophila |
| 73 | 105 | 4.3 | 880 | 1 BRC4_DROME | Q24206 drosophila |
| 74 | 104 | 4.2 | 402 | 1 KAS2_STRCM | P41176 streptomyce |
| 75 | 104 | 4.2 | 1063 | 1 SPT5_YEAST | P27692 saccharomyc |
| 76 | 103.5 | 4.2 | 494 | 1 AMYR_DROLN | O76262 drosophila |
| 77 | 103.5 | 4.2 | 532 | 1 ZIC2_HUMAN | O95409 homo sapien |
| 78 | 103.5 | 4.2 | 975 | 1 CUT1_CANFA | P39881 canis famil |
| 79 | 102.5 | 4.2 | 465 | 1 FXD3_MOUSE | Q61060 mus musculu |
| 80 | 102.5 | 4.2 | 1083 | 1 T2D3_HUMAN | O00268 homo sapien |
| 81 | 101.5 | 4.1 | 497 | 1 FXD2_HUMAN | O60548 homo sapien |
| 82 | 101.5 | 4.1 | 664 | 1 PKND_MYCTU | O05871 mycobacteri |
| 83 | 100.5 | 4.1 | 2647 | 1 FLNA_HUMAN | P21333 homo sapien |
| 84 | 100 | 4.1 | 825 | 1 ICP0_HSV2H | P28284 herpes simp |
| 85 | 99.5 | 4.0 | 1004 | 1 IF2_CORGL | Q8np40 corynebacte |
| 86 | 99.5 | 4.0 | 2647 | 1 FLNA_MOUSE | Q8btm8 mus musculu |
| 87 | 98.5 | 4.0 | 170 | 1 FGFM_HUMAN | Q9hct0 homo sapien |
| 88 | 98 | 4.0 | 933 | 1 NPA3_HUMAN | Q8ixf0 homo sapien |
| 89 | 98 | 4.0 | 964 | 1 IF2_COREF | Q8fpa7 corynebacte |
| 90 | 98 | 4.0 | 1061 | 1 OAR_MYXXA | P38370 myxococcus |
| 91 | 98 | 4.0 | 1376 | 1 VCAP_HSVVB | P28920 equine herp |
| 92 | 97.5 | 3.9 | 494 | 1 AMYR_DROPN | O77022 drosophila |
| 93 | 97.5 | 3.9 | 494 | 1 AMYR_DROSR | O76459 drosophila |
| 94 | 97.5 | 3.9 | 553 | 1 FXC1_MOUSE | Q61572 mus musculu |
| 95 | 97.5 | 3.9 | 972 | 1 OMB_DROME | Q24432 drosophila |
| 96 | 97.5 | 3.9 | 1171 | 1 TR12_STRCO | Q9rkb9 streptomyce |
| 97 | 97 | 3.9 | 493 | 1 AMYR_DROME | O18408 drosophila |
| 98 | 97 | 3.9 | 519 | 1 GAGA_DROME | Q08605 drosophila |
| 99 | 97 | 3.9 | 808 | 1 SYFB_BACHD | Q9k896 bacillus ha |
| 100 | 96.5 | 3.9 | 410 | 1 BHB3_MOUSE | Q99pv5 mus musculu |
| 101 | 96.5 | 3.9 | 495 | 1 PO33_MOUSE | P31361 mus musculu |
| 102 | 96.5 | 3.9 | 1487 | 1 ICP4_HSVVB | P28925 equine herp |
| 103 | 96.5 | 3.9 | 1487 | 1 ICP4_HSVBK | P17473 equine herp |
| 104 | 96 | 3.9 | 494 | 1 AMYR_DROBA | O77019 drosophila |
| 105 | 96 | 3.9 | 500 | 1 PO33_HUMAN | P20264 homo sapien |
| 106 | 95.5 | 3.9 | 431 | 1 UL61_HCMVA | P16818 human cytom |

| | | | | | |
|-----|------|-----|------|---|------------|
| 107 | 95.5 | 3.9 | 475 | 1 | EVX2_MOUSE |
| 108 | 95.5 | 3.9 | 908 | 1 | SRCA_RABIT |
| 109 | 95 | 3.8 | 494 | 1 | AMVR_DROJA |
| 110 | 95 | 3.8 | 530 | 1 | ZIC2_MOUSE |
| 111 | 95 | 3.8 | 825 | 1 | 5E5_RAT |
| 112 | 95 | 3.8 | 904 | 1 | DPO1_MYCTU |
| 113 | 95 | 3.8 | 1120 | 1 | STFR_ECOLI |
| 114 | 95 | 3.8 | 1181 | 1 | ITA7_HUMAN |
| 115 | 94.5 | 3.8 | 375 | 1 | PROB_STRAW |
| 116 | 94.5 | 3.8 | 454 | 1 | YJ45_MYCTU |
| 117 | 93.5 | 3.8 | 342 | 1 | HXD9_HUMAN |
| 118 | 93.5 | 3.8 | 358 | 1 | KLFI_MOUSE |
| 119 | 93.5 | 3.8 | 506 | 1 | THA_PIG |
| 120 | 93.5 | 3.8 | 558 | 1 | YJ83_MYCTU |
| 121 | 93.5 | 3.8 | 641 | 1 | EBN1_EBV |
| 122 | 93.5 | 3.8 | 1336 | 1 | NME4_HUMAN |
| 123 | 93.5 | 3.8 | 1733 | 1 | VNUA_PRVKA |
| 124 | 93 | 3.8 | 506 | 1 | TDT_CHICK |
| 125 | 93 | 3.8 | 880 | 1 | SYA_CAUCK |
| 126 | 92.5 | 3.7 | 276 | 1 | AFRP_STRGR |
| 127 | 92.5 | 3.7 | 492 | 1 | NOA2_HUMAN |
| 128 | 92.5 | 3.7 | 497 | 1 | PO33_RAT |
| 129 | 92.5 | 3.7 | 1333 | 1 | ELF1_DROME |
| 130 | 92.5 | 3.7 | 1380 | 1 | SPI4_YEAST |
| 131 | 92 | 3.7 | 339 | 1 | HXD9_MOUSE |
| 132 | 92 | 3.7 | 633 | 1 | RPOC_CYACA |
| 133 | 92 | 3.7 | 1237 | 1 | B3A2_RABIT |
| 134 | 92 | 3.7 | 1616 | 1 | SLAP_BACCI |
| 135 | 91.5 | 3.7 | 501 | 1 | AMPA_BUCBP |
| 136 | 91.5 | 3.7 | 550 | 1 | CCF_DROME |
| 137 | 91.5 | 3.7 | 639 | 1 | HS74_PARLI |
| 138 | 91.5 | 3.7 | 708 | 1 | JIP1_RAT |
| 139 | 91.5 | 3.7 | 1446 | 1 | IE18_PRVKA |
| 140 | 91 | 3.7 | 780 | 1 | PRTP_HSV1F |
| 141 | 90.5 | 3.7 | 466 | 1 | NRAM_INBMD |
| 142 | 90.5 | 3.7 | 694 | 1 | TKT1_RHIME |
| 143 | 90.5 | 3.7 | 707 | 1 | JIP1_MOUSE |
| 144 | 90.5 | 3.7 | 1461 | 1 | IE18_PRVIF |
| 145 | 90 | 3.6 | 333 | 1 | HME2_HUMAN |
| 146 | 90 | 3.6 | 539 | 1 | CH61_STRAL |
| 147 | 90 | 3.6 | 743 | 1 | TEX3_HUMAN |
| 148 | 90 | 3.6 | 979 | 1 | RFX1_HUMAN |
| 149 | 90 | 3.6 | 1387 | 1 | PUR4_ARATH |
| 150 | 89.5 | 3.6 | 303 | 1 | TAM_STRCO |

ALIGNMENTS

RESULT 1
SHH_HUMAN
ID SHH_HUMAN STANDARD; PRT; 462 AA.
AC Q15465;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sonic hedgehog protein precursor (SHH) (HHG-1).
GN SHH.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal lung;
RX MEDLINE=96070431; PubMed=7590746;
RA Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T., Seidman C.E.,
RA Gastier J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Tabin C.,
RA Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.;
RT "Cloning, expression, and chromosomal location of SHH and IHH: two
RT human homologues of the Drosophila segment polarity gene hedgehog.";
RL Genomics 28:44-51(1995).
RN [2]

RP SEQUENCE FROM N.A.
RA Tate G., Kishimoto K., Mitsuya T.;
RT "Expression of Sonic hedgehog and its receptor Patched/Smoothed in
RT human cancer cell lines and embryonic organs.";
RN J. Biochem. Mol. Biol. Biophys. 4:27-34(2000).
RN [3]
RP SEQUENCE OF 1-197 FROM N.A.
RA Strong C., Graves T., Sutterer C., Ozersky P.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 119-167 FROM N.A.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, genetic linkage and limb patterning activity of a murine
RT hedgehog gene.";
RL Development 120:3339-3353(1994).
RN [5]
RP PALMITOYLATION.
RX MEDLINE=98256339; PubMed=9593755;
RA Pepinsky R.B., Zeng C., Wen D., Rayhorn P., Baker D.P., Williams K.P.,
RA Bixler S.A., Ambrose C.M., Garber E.A., Miatkowski K., Taylor F.R.,
RA Wang E.A., Galdes A.;
RT "Identification of a palmitic acid-modified form of human Sonic
RT hedgehog.";
RL J. Biol. Chem. 273:14037-14045(1998).
RN [6]
RP VARIANTS HPE3 ARG-31; GLY-117 AND ARG-117.
RX MEDLINE=97051937; PubMed=8896572;
RA Roessler E., Belloni E., Gaudenz K., Jay P., Berta P., Scherer S.W.,
RA Tsui L.-C., Muenke M.;
RT "Mutations in the human Sonic hedgehog gene cause holoprosencephaly.";
RL Nat. Genet. 14:357-360(1996).
RN [7]
RP VARIANTS HPE3 ARG-31; GLY-117; ARG-117; GLU-224; THR-226 AND THR-383.
RX MEDLINE=98027056; PubMed=9302262;
RA Roessler E., Belloni E., Gaudenz K., Vargas F., Scherer S.W.,
RA Tsui L.-C., Muenke M.;
RT "Mutations in the C-terminal domain of Sonic hedgehog cause
RT holoprosencephaly.";
RL Hum. Mol. Genet. 6:1847-1853(1997).
RN [8]
RP VARIANTS HPE3 HIS-100; GLN-188 AND ASN-222.
RX MEDLINE=99371775; PubMed=10441331;
RA Odent S., Atti-Bitach T., Blayau M., Mathieu M., Aug J.,
RA Delezo de A.L., Gall J.Y., Le Marec B., Munnich A., David V.,
RA Vekemans M.;
RT "Expression of the Sonic hedgehog (SHH) gene during early human
RT development and phenotypic expression of new mutations causing
RT holoprosencephaly.";
RL Hum. Mol. Genet. 8:1683-1689(1999).
RN [9]
RP VARIANTS HPE3 VAL-88; LYS-115; ARG-236; 263-ARG--ALA-269 DEL; ASP-290;
RX ALA-424 AND LEU-436.
RX MEDLINE=20025757; PubMed=10556296;
RA Nanni L., Ming J.E., Boccian M., Steinhaus K., Bianchi D.W.,
RA Die-Smulders C., Giannotti A., Imaizumi K., Jones K.L., Campo M.D.,
RA Martin R.A., Meinecke P., Pierpont M.E.M., Robin N.H., Young I.D.,
RA Roessler E., Muenke M.;
RT "The mutational spectrum of the sonic hedgehog gene in
RT holoprosencephaly: SHH mutations cause a significant proportion of
RT autosomal dominant holoprosencephaly.";
RL Hum. Mol. Genet. 8:2479-2488(1999).
CC -1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
CC ASSOCIATION WITH SMOOTHED (SMO), TO ACTIVATE THE TRANSCRIPTION
CC OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSSES THE
CC CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER
CC TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A
CC VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED
CC BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE
CC AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
CC ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH
CC FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD

CC CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
CC 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed in fetal intestine, liver, lung, and
CC kidney. Not expressed in adult tissues.

CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).

CC -!- DISEASE: Defects in SHH are the cause of holoprosencephaly 3
CC (HPE3) [MIM:142945]. HPE3 is a clinically variable and genetically
CC heterogeneous malformation in which the developing forebrain fails
CC to correctly separate into right and left hemispheres. HPE3 is
CC associated with several distinct facies and phenotypic
CC variability. In the most extreme cases, anophthalmia or cyclopia
CC is evident along with a congenital absence of the mature nose. The
CC less severe form features facial dysmorphism characterized by
CC ocular hypertelorism, defects of the upper lip and/or nose, and
CC absence of the olfactory nerves or corpus callosum. The majority
CC of HPE3 cases are apparently sporadic, although clear examples of
CC autosomal dominant inheritance have been described. Interestingly,
CC up to 30% of obligate carriers of HPE3 gene in autosomal dominant
CC pedigrees are clinically unaffected.

CC -!- SIMILARITY: Belongs to the hedgehog family.

CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/SHHID378.html".

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CC or send an email to license@isb-sib.ch).

DR EMBL; L38518; AAA62179.1; -.
DR EMBL; AC002484; AAB67604.1; -.
DR HSSP; Q62226; 1VHH.
DR MEROPS; C46.002; -.
DR Genew; HGNC:10848; SHH.
DR MIM; 600725; -.
DR MIM; 142945; -.
DR GO; GO:0007500; P:mesoderm cell fate determination; TAS.
DR GO; GO:0007418; P:ventral midline development; TAS.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR001767; Pept_C46_hint.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PRO0632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS00817; INTEIN_N_TER; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate; Disease mutation; Holoprosencephaly.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 462 SONIC HEDGEHOG PROTEIN.
FT CHAIN 24 197 SONIC HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 198 462 SONIC HEDGEHOG PROTEIN C-PRODUCT.

| | | | | |
|--|-----------|--|------|---|
| FT | DOMAIN | 407 | 411 | POLY-GLY. |
| FT | SITE | 197 | 198 | CLEAVAGE (AUTO-) (BY SIMILARITY). |
| FT | SITE | 243 | 243 | INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY). |
| FT | SITE | 267 | 267 | INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | ACT_SITE | 270 | 270 | ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | LIPID | 24 | 24 | N-palmitoyl cysteine. |
| FT | LIPID | 197 | 197 | Cholesterol glycine ester (By similarity). |
| FT | VARIANT | 31 | 31 | G -> R (in HPE3). |
| FT | VARIANT | 88 | 88 | /FTID=VAR_003619. |
| FT | VARIANT | 100 | 100 | D -> V (in HPE3; familial). |
| FT | VARIANT | 115 | 115 | /FTID=VAR_009163. |
| FT | VARIANT | 117 | 117 | Q -> H (in HPE3; sporadic). |
| FT | VARIANT | 117 | 117 | /FTID=VAR_009164. |
| FT | VARIANT | 188 | 188 | N -> K (in HPE3; familial). |
| FT | VARIANT | 117 | 117 | /FTID=VAR_009165. |
| FT | VARIANT | 117 | 117 | W -> G (in HPE3). |
| FT | VARIANT | 117 | 117 | /FTID=VAR_003620. |
| FT | VARIANT | 188 | 188 | W -> R (in HPE3). |
| FT | VARIANT | 222 | 222 | /FTID=VAR_003621. |
| FT | VARIANT | 224 | 224 | E -> Q (in HPE3; familial). |
| FT | VARIANT | 226 | 226 | /FTID=VAR_009166. |
| FT | VARIANT | 226 | 226 | D -> N (in HPE3; familial). |
| FT | VARIANT | 236 | 236 | /FTID=VAR_009167. |
| FT | VARIANT | 236 | 236 | V -> E (in HPE3). |
| FT | VARIANT | 226 | 226 | /FTID=VAR_009168. |
| FT | VARIANT | 236 | 236 | A -> T (in HPE3; familial). |
| FT | VARIANT | 236 | 236 | /FTID=VAR_009169. |
| FT | VARIANT | 236 | 236 | S -> R (in HPE3; familial). |
| Query Match 97.5%; Score 2407; DB 1; Length 462; | | | | |
| Best Local Similarity 100.0%; Pred. No. 2.1e-166; | | | | |
| Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| Qy | 1 | MLLLARCLLLLVSSLLVCSGLACGPGRGKRRHPKLTPLAYKQIPNVAEKTILGASG | 60 | |
| Db | 1 | MLLLARCLLLLVSSLLVCSGLACGPGRGKRRHPKLTPLAYKQIPNVAEKTILGASG | 60 | |
| Qy | 61 | RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV | 120 | |
| Db | 61 | RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQPGV | 120 | |
| Qy | 121 | KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH | 180 | |
| Db | 121 | KLRVTEGWDEDDHHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYYESKAH | 180 | |
| Qy | 181 | IHCsvKAENsvAAKSGGCGPGSATVHLEQGQTKLVKDLSPGDRVLAADDQGRLLYSDFLT | 240 | |
| Db | 181 | IHCsvKAENsvAAKSGGCGPGSATVHLEQGQTKLVKDLSPGDRVLAADDQGRLLYSDFLT | 240 | |
| Qy | 241 | FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG | 300 | |
| Db | 241 | FLDRDDGAKKVFYVETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALG | 300 | |
| Qy | 301 | PRALFASRVPGQVRVYVAERDGRRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL | 360 | |
| Db | 301 | PRALFASRVPGQVRVYVAERDGRRLLPAAVHVSVTLSSEAAGAYAPLTAQGTILINRVL | 360 | |
| Qy | 361 | ASCVAVIEHSHWAHRAFAFRLAHALLAALAPARTIDRGDGGGDRGGGRVALTAPGA | 420 | |
| Db | 361 | ASCVAVIEHSHWAHRAFAFRLAHALLAALAPARTIDRGDGGGDRGGGRVALTAPGA | 420 | |
| Qy | 421 | ADAPGAGATAGIHWYSQLYQIGTWLLDSEALHPLGMVAVKSS | 462 | |
| Db | 421 | ADAPGAGATAGIHWYSQLYQIGTWLLDSEALHPLGMVAVKSS | 462 | |
| RESULT 2 | | | | |
| SHH_MOUSE | | | | |
| ID | SHH_MOUSE | STANDARD; | PRT; | 437 AA. |

AC Q62226;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sonic hedgehog protein precursor (SHH) (HHG-1).
GN SHH OR HHG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=94094334; PubMed=7916661;
RA Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J.,
RA McMahon J.A., McMahon A.P.;
RT "Sonic hedgehog, a member of a family of putative signaling
RT molecules, is implicated in the regulation of CNS polarity.";
RL Cell 75:1417-1430(1993).
RN [2]
RP REVISION TO 122.
RC STRAIN=C57BL/6J;
RA McMahon A.P.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, genetic linkage and limb patterning activity of a murine
RT hedgehog gene.";
RL Development 120:3339-3353(1994).
RN [4]
RP FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.
RX MEDLINE=95254654; PubMed=7736596;
RA Roelink H., Porter J.A., Chiang C., Tanabe Y., Chang D.T.,
RA Beachy P.A., Jessell T.M.;
RT "Floor plate and motor neuron induction by different concentrations of
RT the amino-terminal cleavage product of sonic hedgehog
RT autoproteolysis.";
RL Cell 81:445-455(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 34-195.
RX MEDLINE=96069744; PubMed=7477329;
RA Hall T.M.T., Porter J.A., Beachy P.A., Leahy D.J.;
RT "A potential catalytic site revealed by the 1.7-A crystal structure of
RL the amino-terminal signalling domain of Sonic hedgehog.";
CC -1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
CC ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION
CC OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSSES THE
CC CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER
CC TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A
CC VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED
CC BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE
CC AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
CC ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH
CC FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD
CC CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
CC 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES
CC INCLUDING THE NOTOCHORD, VENTRAL NEURAL TUBE, FLOOR PLATE, LUNG
CC BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHYME
CC OF LIMES. IN THE ADULT, EXPRESSED IN LUNG AND NEURAL RETINA.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.
CC -1- INDUCTION: By retinoic acid.
CC -1- PTM: The C-terminal domain displays an autoproteolysis activity
CC and a cholesterol transferase activity. Both activities result in

CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity.
CC -1- SIMILARITY: Belongs to the hedgehog family.
CC
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CC
CC EMBL; X76290; CAA53922.1; -.
CC PDB; 1VHH; 29-JAN-96.
CC MEROPS; C46.002; -.
CC MGD; MGI:98297; Shh.
CC GO; GO:0007411; P:axon guidance; IDA.
CC GO; GO:0001708; P:cell fate specification; IMP.
CC GO; GO:0007417; P:central nervous system development; IMP.
CC GO; GO:0001747; P:eye morphogenesis (sensu Mammalia); IMP.
CC GO; GO:0001654; P:eye morphogenesis; IDA.
CC GO; GO:0030539; P:male genital morphogenesis; IMP.
CC GO; GO:0007389; P:pattern specification; IMP.
CC GO; GO:0042127; P:regulation of cell proliferation; IDA.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR003587; Hedgehog_hint_N.
CC InterPro; IPR003586; Hedgehog_hint_C.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR006141; Intein_S.
CC InterPro; IPR001767; Pept_C46_hint.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC Pfam; PF01079; Hint; 1.
CC PRINTS; PR00632; SONICHHOG.
CC ProDom; PD003042; HH_signal; 1.
CC SMART; SM00305; HintC; 1.
CC SMART; SM00306; HintN; 1.
CC PROSITE; PS50817; INTEIN_N_TER; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate; 3D-structure.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 437 SONIC HEDGEHOG PROTEIN.
FT CHAIN 25 198 SONIC HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 199 437 SONIC HEDGEHOG PROTEIN C-PRODUCT.
FT DOMAIN 383 387 POLY-GLY.
FT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY). (BY
FT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY
FT SITE 268 268 SIMILARITY).
FT ACT_SITE 271 271 INVOLVED IN AUTO-CLEAVAGE (BY
FT ACT_SITE 271 271 SIMILARITY).
FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY
FT LIPID 25 25 SIMILARITY).
FT LIPID 198 198 N-palmitoyl cysteine (By similarity).
FT TURN 45 46 Cholesterol glycine ester (By
FT STRAND 48 49 similarity).
FT TURN 54 55
FT TURN 57 60
FT TURN 69 70
FT HELIX 72 76
FT STRAND 78 79
FT TURN 83 84
FT STRAND 85 87
FT TURN 90 91
FT HELIX 95 97
FT STRAND 98 99
FT HELIX 101 117

FT LIPID 25 25 N-palmitoyl cysteine (By similarity).
FT LIPID 198 198 Cholesterol glycine ester (By
FT LIPID 198 198 similarity).
SQ SEQUENCE 437 AA; 47630 MW; 0DFC19F0D1662A0 CRC64;
Query Match 83.4%; Score 2060; DB 1; Length 437;
Best Local Similarity 87.5%; Pred. No. 2.2e-141;
Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;
QY 1 MLLARCLLLVSSLLVCSGLACGFGKRRHPKLTPLAYKQFIPNVAEKLGSAG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2 LLLARCFVLALASSLLVCPGLACGFGKRRHPKLTPLAYKQFIPNVAEKLGSAG 61
QY 61 RYEGKISRNSERFKELTPNYPDIFKDEENTGADRLMTQRCCKLNALAISSVNWQPGV 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 RYEGKITRNSERFKELTPNYPDIFKDEENTGADRLMTQRCCKLNALAISSVNWQPGV 121
QY 121 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRSKYGNLARLAVEAGFDVWVYESKAH 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
122 KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRSKYGNLARLAVEAGFDVWVYESKAH 181
QY 181 IHCSVKAENSVAAKSGGCGFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
182 IHCSVKAENSVAAKSGGCGFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
QY 241 FLDRDGAQKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGCALG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
242 FLDRDGAQKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGCALG 300
QY 301 PRALFASRVPRQGVVVAERDGRRLPAAVSHVTLSEEAAGAYAPLTAQGTILINRVL 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
287 PSPLFASRVPRQGVVVAERDGRRLPAAVSHVTLSEEAAGAYAPLTAQGTILINRVL 346
QY 361 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAP-G 419
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
347 ASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGRVALTAP-G 419
QY 420 AADAPGAGATAGIHWYSQQLYQIGTWLLDSEALHPLGMVAKSS 462
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
395 VAEARGAGPPAGIHWYSQQLYHIGTWLLDSETLHPLGMVAKSS 437

RESULT 4
SHH_CHICK STANDARD; PRT; 425 AA.
AC Q91035; 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sonic hedgehog protein precursor (SHH).
GN SHH.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb bud;
RX MEDLINE=94094333; PubMed=8269518;
RA Riddle R.D., Johnson R.L., Laufer E., Tabin C.;
RT "Sonic hedgehog mediates the polarizing activity of the ZPA.";
RL Cell 75:1401-1416(1993).
[2]
RN FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.
RP MEDLINE=95254654; PubMed=7736596;
RX Roelink H., Porter J.A., Chiang C., Tanabe Y., Chang D.T.,
RA Beachy P.A., Jessell T.M.;
RT "Floor plate and motor neuron induction by different concentrations of
RT the amino-terminal cleavage product of sonic hedgehog
RT autoproteolysis.";
RL Cell 81:445-455(1995).

-|- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
ASSOCIATION WITH SMOOTHED (SMO), TO ACTIVATE THE TRANSCRIPTION
OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSSES THE
CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER
TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A
VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED
BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE
AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH
FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD
CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION.
-|- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
-|- TISSUE SPECIFICITY: EXPRESSED IN THE POSTERIOR LIMB BUD
MESENCHYME, THE HENSEN'S NODE, THE NOTOCHORD, AND THE FLOOR PLATE
OF THE NEURAL TUBE.
-|- DEVELOPMENTAL STAGE: FIRST DETECTABLE AT STAGE 17 DURING THE
INITIATION OF LIMB BUD FORMATION. FROM THAT POINT ONWARDS, THE
EXPRESSION PATTERN EXACTLY MATCHES THE LOCATION OF THE ZONE OF
POLARIZING ACTIVITY (ZPA).
-|- INDUCTION: By retinoic acid.
-|- PTM: The C-terminal domain displays an autoproteolysis activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity.
-|- SIMILARITY: Belongs to the hedgehog family.

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or send an email to license@isb-sib.ch).

EMBL; L28099; AAA72428.1; --
PIR; A49424; A49424.
HSSP; Q62226; 1VHH.
MEROPS; C46.001; --
InterPro; IPR009045; Hedgehog/DD_pept.
InterPro; IPR003587; Hedgehog_hint_N.
InterPro; IPR003586; Hedgehog_hintC.
InterPro; IPR000320; HH_signal.
InterPro; IPR006141; Intein_S.
InterPro; IPR001767; Pept_C46_hint.
Pfam; PF01085; HH_signal; 1.
Pfam; PF01079; Hint; 1.
PRINTS; PR00632; SONICHOG.
ProDom; PD003042; HH_signal; 1.
SMART; SM00305; HintC; 1.
SMART; SM00306; HintN; 1.
PROSITE; PS50817; INTEIN_N_TER; 1.
Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
Signal; Lipoprotein; Palmitate.
SIGNAL 1 26 POTENTIAL.
CHAIN 27 425 SONIC HEDGEHOG PROTEIN.
CHAIN 27 200 SONIC HEDGEHOG PROTEIN N-PRODUCT.
CHAIN 201 425 SONIC HEDGEHOG PROTEIN C-PRODUCT.
DOMAIN 390 393 POLY-THR.
SITE 200 201 CLEAVAGE (AUTO-) (PROBABLE).
SITE 246 246 INVOLVED IN CHOLESTEROL TRANSFER (BY
SIMILARITY).
SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY
SIMILARITY).

| | | | | |
|-----------------------|--|---|----------------|--|
| FT | ACT_SITE | 273 | 273 | ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | LIPID | 27 | 27 | N-palmitoyl cysteine (By similarity). |
| FT | LIPID | 200 | 200 | Cholesterol glycine ester (By similarity). |
| SQ | SEQUENCE | 425 AA; 46474 MW; DA9627443D4A0173 CRC64; | | |
| Query Match | | | | |
| Best Local Similarity | | 73.2%; | Score 1807; | DB 1; Length 425; |
| Matches 361; | | Conservative 22; | Mismatches 37; | Indels 44; Gaps 6; |
| QY | 1 | MLLLARCLLLVLVSSLLVCSGLACGPGRRGKRRHPKLTPLAYKQFIPNVAEKTLGASG | 60 | |
| Db | 4 | MLLLTRILLVGFICALLVSSGLTCGPGRGIGKRRHPKLTPLAYKQFIPNVAEKTLGASG | 63 | |
| QY | 61 | RYEGKISRNSERFKELTPNYPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV | 120 | |
| Db | 64 | RYEGKITRNSERFKELTPNYPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV | 123 | |
| QY | 121 | KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGEDWVYESKAH | 180 | |
| Db | 124 | KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGEDWVYESKAH | 183 | |
| QY | 181 | IHCSVKAENSVAKSGGCFPGSATVHLEQGCTKLVKDLSPGDRVLAADDQGRLLYSDELT | 240 | |
| Db | 184 | IHCSVKAENSVAKSGGCFPGSATVHLEHGGCTKLVKDLSPGDRVLAADDQGRLLYSDELT | 243 | |
| QY | 241 | FLDRDDGAKKVFYIETREPRERLLLTAAHLFVAP-HNDS-ATGEPEASSGSGPPSGGA | 298 | |
| Db | 244 | FLDRMDSSRKLFYIETROPRARLLLTAAHLFVAPQHNQSEATG-----STSG----- | 292 | |
| QY | 299 | LGPRALFASRVRCQRVVVAERDGRRLPAAVSHSVTLSEEAAGAYAPLTAQGTILINR | 358 | |
| Db | 293 | ---QALFASNVKPGQRVVVLGE--GGQQLLPASVHSVLSREASGAYAPLTAQGTILINR | 347 | |
| QY | 359 | VLASCYAVIEHSHWAHRAFAFRLAHALLAALAPARTDRGGDSGGDRGGGRVALTAP | 418 | |
| Db | 348 | VLASCYAVIEHSHWAHRAFAFRLAQGLLAL-----CP | 381 | |
| QY | 419 | GAADAPGAGATAGIHWYSQLLYQIGTWLDDSEALHPLGMVKSS | 462 | |
| Db | 382 | DGAIPTAATTTTGTHWYSRLLYRIGSWVLDDGALHPLGMVAPAS | 425 | |
| RESULT 5 | | | | |
| SHH_CYNPY | SHH_CYNPY | STANDARD; | PRT; | 432 AA. |
| AC | Q90385; | | | |
| DT | 15-JUL-1999 | (Rel. 38, Created) | | |
| DT | 15-JUL-1999 | (Rel. 38, Last sequence update) | | |
| DT | 10-OCT-2003 | (Rel. 42, Last annotation update) | | |
| DE | Sonic hedgehog protein precursor (SHH). | | | |
| GN | SHH. | | | |
| OS | Cynops pyrrhogaster (Japanese common newt). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops. | | | |
| OX | NCBI_TaxID=8330; | | | |
| RN | [1] | | | |
| RF | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Embryo; | | | |
| RX | MEDLINE=96136334; PubMed=8573168; | | | |
| RA | Takabatake T., Takahashi T.C., Inoue K., Ogawa M., Takeshima K.; | | | |
| RT | "Activation of two Cynops genes, fork head and sonic hedgehog, in animal cap explants."; | | | |
| RL | Biochem. Biophys. Res. Commun. 218:395-401(1996). | | | |
| CC | -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY | | | |
| CC | SIMILARITY). | | | |
| CC | -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity). | | | |
| CC | -!- INDUCTION: ACTIVATED BY ACTIVIN, BASIC FIBROBLAST GROWTH FACTOR (BFGF) AND FORK HEAD. | | | |
| CC | -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity). | | | |
| CC | -!- SIMILARITY: Belongs to the hedgehog family. | | | |
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| CC | EMBL; D63339; BAA09657.1; -. | | | |
| DR | HSSP; Q62226; 1VHH. | | | |
| DR | MEROPS; C46.002; -. | | | |
| DR | InterPro; IPR009045; Hedgehog/DD_pept. | | | |
| DR | InterPro; IPR003587; Hedgehog_hint_N. | | | |
| DR | InterPro; IPR003586; Hedgehog_hint_C. | | | |
| DR | InterPro; IPR000320; HH_signal. | | | |
| DR | InterPro; IPR006141; Intein_S. | | | |
| DR | InterPro; IPR001767; Pept_C46_hint. | | | |
| DR | InterPro; IPR001657; Peptidase_C46. | | | |
| DR | Pfam; PF01085; HH_signal; 1. | | | |
| DR | Pfam; PF01079; Hint; 1. | | | |
| DR | PRINTS; PR00632; SONICHOG. | | | |
| DR | ProDom; PD003042; HH_signal; 1. | | | |
| DR | SMART; SM00305; HintC; 1. | | | |
| DR | SMART; SM00306; HintN; 1. | | | |
| DR | PROSITE; PS00817; INTEIN_N_TER; 1. | | | |
| KW | Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; | | | |
| KW | Signal; Lipoprotein; Palmitate. | | | |
| FT | SIGNAL | 1 | 26 | POTENTIAL. |
| FT | CHAIN | 27 | 432 | SONIC HEDGEHOG PROTEIN. |
| FT | CHAIN | 27 | 200 | SONIC HEDGEHOG PROTEIN N-PRODUCT. |
| FT | CHAIN | 201 | 432 | SONIC HEDGEHOG PROTEIN C-PRODUCT. |
| FT | SITE | 200 | 201 | CLEAVAGE (AUTO-) (BY SIMILARITY). |
| FT | SITE | 268 | 268 | INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | ACT_SITE | 271 | 271 | ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | LIPID | 27 | 27 | N-palmitoyl cysteine (By similarity). |
| FT | LIPID | 200 | 200 | Cholesterol glycine ester (By similarity). |
| SQ | SEQUENCE | 432 AA; 47847 MW; B455C7E746C8E5A8 CRC64; | | |
| Query Match | | | | |
| Best Local Similarity | | 62.4%; | Score 1539.5; | DB 1; Length 432; |
| Matches 325; | | Conservative 36; | Mismatches 75; | Indels 39; Gaps 8; |
| QY | 1 | MLLLARCLLLVLVSSLLVCSGLACGPGRRGKRRHPKLTPLAYKQFIPNVAEKTLGASG | 60 | |
| Db | 4 | MLLLRRVLLAGFICALVPSGLSCGPGRGIGTRFKRKKLTPLAYKQFTPNVPEKTLGASG | 63 | |
| QY | 61 | RYEGKISRNSERFKELTPNYPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV | 120 | |
| Db | 64 | RYEGKITRNSERFKELTPNYPNPDIIFKDEENTGADRLMTQRCCKLNALAI SVMNQWPGV | 123 | |
| QY | 121 | KLRVTEGWDEDDHSEESLHYEGRAVDITTSDDRSKYGMLARLAVEAGEDWVYESKAH | 180 | |

Db 124 KLRVTGWDGDGHFEESLHYEGRAVDITTSDDRRSKYGMRLARLAAEAGFDWVYFESKAH 183

QY 181 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAAADDQGRLLYSDFLT 240

Db 184 IHCSVKAENSVAAKSGGCFPGSATVALEQGVRIPVKDLRPGDRVLAAADGLKLVYSDFLL 243

QY 241 FLDRDDCAKKVFYVIETREPERLLLTAAHLLFVA---PHNDSATGEPEASSGSGPPSGG 297

Db 244 FMDKEETVRKVYFIET--SRERVRLTAHLLFVQGAHGND-----SGGDFRSVFG 293

QY 298 ALGPRALPASRVPRGQRVYVVAERDGDORLLPAAVSHSVTLSEEAAGAYAPLTAQGTILIN 357

Db 294 SAGFRSMFASSVRAGRHLTV-DREG-RGLREATVERVYL-EEATGAYAPVTAHGTVID 350

QY 358 RVLASCYAVIEHSHWAHRAFAPEFLAHALLAALAPARTDRGGDSGGDRGGGGRVALTA 417

Db 351 RVLASCYAVIEHSHWAHWAFAPLRVCLGILSFESP--QDYSSHS----- 392

QY 418 PGAADAPGAGATAGIHWYSQLLYQIGTWLLDSEALHPLGNVAVKSS 462

Db 393 -----PPAPSQSEGVHWYSEILYRIGTWVLQEDTIHPLGNAKSS 432

RESULT 6

SHH_BRARE STANDARD; PRT; 418 AA.

AC Q92008; O13170; O13171;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sonic hedgehog protein precursor (SHH) (VHH-1).

GN SHH OR VHH1.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=94170375; PubMed=8124714;

RA Roelink H., Augsburg A., Heemskerk J., Korzh V., Norlin S.,

RA Ruiz i Altaba A., Tanabe Y., Placzek M., Edlund T., Jessell T.M.,

RA Dodd J.;

RT "Floor plate and motor neuron induction by vhh-1, a vertebrate homolog

RT of hedgehog expressed by the notochord.";

RL Cell 76:761-775(1994).

RN [2]

RP SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.

RX MEDLINE=96014264; PubMed=7583153;

RA Ekker S.C., Ungar A.R., Greenstein P., von Kessler D.P., Porter J.A.,

RA Moon R.T., Beachy P.A.;

RT "Patterning activities of vertebrate hedgehog proteins in the

RT developing eye and brain.";

RL Curr. Biol. 5:944-955(1995).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=96083328; PubMed=7579523;

RA Fietz M.J., Concordet J.-P., Barbosa R., Johnson R., Krauss S.,

RA McMahon A.P., Tabin C., Ingham P.W.;

RT "The hedgehog gene family in Drosophila and vertebrate development.";

RL Development Suppl. 43:51(1994).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=99225458; PubMed=10207136;

RA Muller F., Chang B., Albert S., Fischer N., Tora L., Strahle U.;

RA "Intrinsic enhancers control expression of zebrafish sonic hedgehog in

RT floor plate and notochord.";

RL Development 126:2103-2116(1999).

RN [5]

RP SEQUENCE OF 30-92 AND 113-170 FROM N.A.

RC TISSUE=Muscle;

RX MEDLINE=97075114; PubMed=8917540;

RA Zardoya R., Abouheif E., Meyer A.;

RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species

RT closely related to the zebrafish.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).

CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF

CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE

CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING

CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS

CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)

CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO

CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,

CC PTC REPRESENTS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY

CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the

CC cell, while the N-terminal peptide remains associated with the

CC cell surface. Is also secreted in either cleaved or uncleaved form

CC to mediate signaling to other cells (By similarity).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL

CC TUBE AND BRAIN. ALSO FOUND IN THE NOTOCHORD AND IN DEVELOPING FIN

CC BUD. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT

CC INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON.

CC -!- DEVELOPMENTAL STAGE: FIRST DETECTABLE IN THE INNER CELL LAYER OF

CC THE EMBRYONIC SHIELD DURING GASTRULATION. BY 9.5 HRS OF

CC DEVELOPMENT, EXPRESSED IN A CONTINUOUS BAND THAT EXTENDS FROM THE

CC TAIL TO THE HEAD, THE ANTERIOR BOUNDARY OF EXPRESSION BEING

CC POSITIONED IN THE CENTER OF THE ANIMAL POLE ANTERIOR TO THE

CC PRESUMPTIVE MIDBRAIN.

CC -!- PTM: The C-terminal domain displays an autophosphorylation activity

CC and a cholesterol transferase activity. Both activities result in

CC the cleavage of the full-length protein and covalent attachment of

CC a cholesterol moiety to the C-terminal of the newly generated N-

CC terminal fragment (N-product). This covalent modification appears

CC to play an essential role in restricting the spatial distribution

CC of the protein activity to the cell surface. The N-product is the

CC active species in both local and long-range signaling, whereas the

CC C-product has no signaling activity (By similarity).

CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; L27585; AAA20998.1; -.

CC EMBL; U30711; AAC59742.1; -.

CC EMBL; Z35669; CAA84738.1; -.

CC EMBL; AF124382; AAD47913.1; -.

CC EMBL; U51351; AAB38575.1; -.

CC EMBL; U51370; AAB38593.1; -.

CC PIR; A53193; A53193.

CC HSSP; Q62226; 1VHH.

CC MEROPS; C46.002; -.

CC ZFIN; ZDB-GENE-980526-166; shh.

CC InterPro; IPR009045; Hedgehog/DD_pept.

CC InterPro; IPR003587; Hedgehog_hintN.

CC InterPro; IPR003586; Hedgehog_hintC.

CC InterPro; IPR000320; HH_signal.

CC InterPro; IPR006141; Intein_S.

CC InterPro; IPR001767; Pept_C46_hint.

CC InterPro; IPR001657; Peptidase_C46.

CC Pfam; PF01085; HH_signal; 1.

CC Pfam; PF01079; Hint; 1.

CC PRINTS; PR00632; SONICHHOG.

CC PRODom; PD003042; HH_signal; 1.

CC SMART; SM00305; HintC; 1.

CC SMART; SM00306; HintN; 1.

CC PROSITE; PS50817; INTEIN_N_TER; 1.

CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;

CC Signal; Lipoprotein; Palmitate.

CC SIGNAL 1 23 POTENTIAL.

| | | | | |
|----------|---|--|-------------------|---|
| FT | CHAIN | 24 | 418 | SONIC HEDGEHOG PROTEIN. |
| FT | CHAIN | 24 | 197 | SONIC HEDGEHOG PROTEIN N-PRODUCT. |
| FT | CHAIN | 198 | 418 | SONIC HEDGEHOG PROTEIN C-PRODUCT. |
| FT | SITE | 197 | 198 | CLEAVAGE (AUTO-). |
| FT | SITE | 243 | 243 | INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY). |
| FT | SITE | 267 | 267 | INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | ACT_SITE | 270 | 270 | ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY). |
| FT | LIPID | 24 | 24 | N-palmitoyl cysteine (By similarity). |
| FT | LIPID | 197 | 197 | Cholesterol glycine ester (By similarity). |
| FT | SEQUENCE | 418 AA; | 46402 MW; | CF000AFFFED2F5795 CRC64; |
| Qy | Query Match | 61.0%; | Score 1506; | DB 1; Length 418; |
| Db | Best Local Similarity | 64.5%; | Pred. No. 2e-101; | |
| Db | Matches 300; | Conservative 47; | Mismatches 68; | Indels 50; Gaps 5; |
| Qy | 1 | MLLLARCLLLVSSLLVCSGLACGPGRGKRRHPKLTPLAYKQFIPNVAEKTGLGASG | 60 | |
| Db | 1 | MRLLTRVLLVSLTSLVSVGLACGPGRGYRRRHPKLTPLAYKQFIPNVAEKTGLGASG | 60 | |
| Qy | 61 | RYEGKISRNSERKELTPNYNPDIIFFKDEENTGADRLMTQRCCKLNALAISVMNQPGV | 120 | |
| Db | 61 | RYEGKITRNSERKELTPNYNPDIIFFKDEENTGADRLMTQRCCKLNLSAISVMNHWPV | 120 | |
| Qy | 121 | KLRVTEGWDEGHSEESLHYEGRAVDITSDRRSKYGMRLARLAVEAGFDWVYVESKAH | 180 | |
| Db | 121 | KLRVTEGWDEGHFEESLHYEGRAVDITSDRDKSKYGLTSLRLAVEAGFDWVYVESKAH | 180 | |
| Qy | 181 | IHCsvKAENsvAAKSGGCGFPGSATVHLEQGCTKLVDLSPGDRVLAADDQGRLLYSDFLT | 240 | |
| Db | 181 | IHCsvKAENsvAAKSGGCGFPGSALVSLQGGQKAVKDLNPGDKVLAADSAGNLVFSDFIM | 240 | |
| Qy | 241 | FLDRDDGAKKVFYVETREPRERLLLTAAHLFLVAPHNDSATGEPEASSGSGPPSGGALG | 300 | |
| Db | 241 | FTDRDSTTRRVFYVETQEPVEKITLTAHLLFVL---DNSTEDLHWT----- | 286 | |
| Qy | 301 | PRALFASRVPRGQVYVVAERDGRRLLPAAVHVSVTLSSEAAAGAVAPLTAQGTILINRVL | 360 | |
| Db | 287 | --AAYASSVRAGQKVMV---DDSGQLKSVIVQRIYTEQRGSFAPVTAHGTIVVDRI | 340 | |
| Qy | 361 | ASCYAVIEHSHWAFAPFRLAHALLAALAPARTDRGGDGGDRGGGRVALTAPGA | 420 | |
| Db | 341 | ASCYAVIEDQGLAHAFAPARLYYVVSFLFPQNS----- | 375 | |
| Qy | 421 | ADAPGAGAT---AGIHWYSQLLYQIGTWLLDSEALHPLGMVAVKSS | 462 | |
| Db | 376 | --SSRSNATLQQEGVHWYSRLLYQMGTWLLDSNMLHPLGMSVNSS | 418 | |
| RESULT 7 | SHH_XENLA | STANDARD; | PRT; | 444 AA. |
| AC | Q92000; Q91894; | | | |
| DT | 15-JUL-1999 (Rel. 38, Created) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Sonic hedgehog protein precursor (X-SHH) (VHH-1). | | | |
| GN | SHH. | | | |
| OS | Xenopus laevis (African clawed frog). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; | | | |
| OC | Xenopodinae; Xenopus. | | | |
| OX | NCBI_TaxID=8355; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Intestine; | | | |
| RX | MEDLINE=95357169; PubMed=7630736; | | | |
| RA | Stolow M.A., Shi Y.-B.; | | | |
| RT | "Xenopus sonic hedgehog as a potential morphogen during embryogenesis and thyroid hormone-dependent metamorphosis." | | | |

Nucleic Acids Res. 23:2555-2562(1995).

[2] SEQUENCE FROM N.A.

TISSUE=Embryo;

MEDLINE=95401852; PubMed=7671800;

Egger S.C., McGrew L.L., Lai C.-J., Lee J.J., von Kessler D.P., Moon R.T., Beachy P.A.;

"Distinct expression and shared activities of members of the hedgehog gene family of Xenopus laevis.";

Development 121:2337-2347(1995).

[3] SEQUENCE FROM N.A.

TISSUE=Notochord;

MEDLINE=96028338; PubMed=7551564;

Ruiz i Altaba A., Jessell T.M., Roelink H.;

"Restrictions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";

Mol. Cell. Neurosci. 6:106-121(1995).

-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).

-!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN NOTOCHORD AND NEURAL FLOOR PLATE DURING EMBRYOGENESIS. IN TADPOLE, HIGH EXPRESSION IS OBSERVED IN PANCREAS/STOMACH, MODERATE EXPRESSION IN TAIL, AND LOW EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.

-!- DEVELOPMENTAL STAGE: FIRST DETECTED AT THE NEURULA (STAGES 16-17). FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40). HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES MORPHOGENESIS.

-!- INDUCTION: By thyroid hormone.

-!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).

-!- SIMILARITY: Belongs to the hedgehog family.

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EMBL; L39213; AAC42227.1; -.

EMBL; U26314; AAA85162.1; -.

EMBL; L35248; AAA49981.1; -.

PIR; S56765; S56765.

HSSP; Q62226; 1VHH.

MEROPS; C46.002; -.

InterPro; IPR009045; Hedgehog/DD_pept.

InterPro; IPR003587; Hedgehog hint N.

InterPro; IPR003586; Hedgehog hint C.

InterPro; IPR000320; HH signal.

InterPro; IPR006141; Intein S.

InterPro; IPR001767; Pept C46 hint.

InterPro; IPR001657; PeptIdase_C46.

FT SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY
FT ACT_SITE 273 273 SIMILARITY).
FT ESSENTIAL FOR AUTO-CLEAVAGE (BY
FT SIMILARITY).
FT LIPID 27 27 N-palmitoyl cysteine (By similarity).
FT LIPID 200 200 Cholesterol glycine ester (By
FT similarity).
SQ SEQUENCE 416 AA; 46576 MW; 61EC2218309CFE59 CRC64;
Query Match 58.0%; Score 1432; DB 1; Length 416;
Best Local Similarity 62.6%; Pred. No. 4.4e-96;
Matches 288; Conservative 39; Mismatches 77; Indels 56; Gaps 5;
Qy 2 LLLAPCLLLVSSLLVCSGLACGPGRGFGKRRHPKLTPLAYKQFIPNVAEKTIGASGR 61
Db 5 LHLKQFALLCFISLLLTTPCGLACGPGRGYKRRHPKLTPLAYKQFIPNVAEKTIGASGK 64
Qy 62 YEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGVK 121
Db 65 YEGKITRNSERFKELIPNYPNDIIFKDEENTNADRLMTKRCCKDLNSLAISVMNHWPVK 124
Qy 122 LRVTEGDEDDGHHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAHI 181
Db 125 LRVTEGDEDDGHHLEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAHI 184
Qy 182 HCSVKAENSVAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTF 241
Db 185 HCSVKAENSVAKSGGCGPFGSGVTLDGTRKPIKDLKVGDRVLAADKGNVLISDFIMF 244
Qy 242 LDRDGAKKVPYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGP 301
Db 245 IDHDPTRRQFIVIETSEPTKLTTLTAHLLFVVG--NSSA-----ASGI 286
Qy 302 RALFASVRPQGVVVAERDGRRLLPAAVHSTL-----SEEAAGAYAPLTAQGTILIN 357
Db 287 TATFASNVKPGDVTLVWED-----TCESLKSVTVKRIYTEHEGSPAPVTAHGTIIVD 339
Qy 358 RVLASCYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTA 417
Db 340 QVLASCYAVIENHKWAHWAFAFVRLCHKLTWLFPARESNVNFQ----- 383
Qy 418 PGADAPGAGATAGIHWSYQLLYOIGTWLLDSEALHPLGM 457
Db 384 -----EDGIHWYSNMLFHIGSWLLDRDSFHPLGI 412

RESULT 9
IHH_CHICK
ID_IHH_CHICK STANDARD; PRT; 408 AA.
AC Q98938;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Indian hedgehog protein precursor (IHH).
GN IHH.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96325423; PubMed=8662546;
RA Vortkamp A., Lee K., Lanske B., Segre G.V., Kronenberg H.M.,
RA Tabin C.J.;
RT "Regulation of rate of cartilage differentiation by Indian hedgehog
and PTH-related protein.";
RL Science 273:613-622(1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
CC PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN
CC ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH

CC AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION
CC OF PARATHYROID HORMONE-RELATED PROTEIN (PTHrP).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. Is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND
CC CARTILAGE OF DEVELOPING LONG BONES IN THE LIMB.
CC -!- PFM: The C-terminal domain displays an autoprotoeolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; U58511; AAC60010.1; -.
CC HSSP; Q62226; 1VHH.
CC MEROPS; C46.003; -.
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR003587; Hedgehog_hint_N.
CC InterPro; IPR003586; Hedgehog_hint_C.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001767; Pept_C46_hint.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC Pfam; PF01079; Hint; 1.
CC PRINTS; PR00632; SONICHHOG.
CC ProDom; PD003042; HH_signal; 1.
CC SMART; SM00305; HintC; 1.
CC SMART; SM00306; HintN; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 408 INDIAN HEDGEHOG PROTEIN.
FT CHAIN 24 198 INDIAN HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 199 408 INDIAN HEDGEHOG PROTEIN C-PRODUCT.
FT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY
FT SIMILARITY).
FT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY
FT SIMILARITY).
FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY
FT SIMILARITY).
FT LIPID 24 24 N-palmitoyl cysteine (By similarity).
FT LIPID 198 198 Cholesterol glycine ester (By
FT similarity).
SQ SEQUENCE 408 AA; 44829 MW; BA397AE2A9357A24 CRC64;

Query Match 51.9%; Score 1282.5; DB 1; Length 408;
Best Local Similarity 59.7%; Pred. No. 2.7e-85;
Matches 271; Conservative 34; Mismatches 92; Indels 57; Gaps 8;
Qy 5 ARCLLLVLVSSLLVCSGL-ACGPGRGFG-KRRHPKLTPLAYKQFIPNVAEKTIGASGRY 62
Db 4 ARLLLLSGCALLLAPAVRCGPGRVGSRPPRKLIPLAYKQFSPNVPEKTIGASGRY 63
Qy 63 EGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNALAISVMNQWPGVKL 122
Db 64 EGKIARNSERFKELTPNYPNDIIFKDEENTGADRLMTQRCCKDLNSLAISVMNQWPGVKL 123
Qy 123 RVTEGDEDDGHHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYYESKAHI 182

Db 124 RVTEGWDEGHSESLHYEGRAVDITTSDRNRKYMGLARLAVEAGFDWVYVESKAHIIH 183
QY 183 CSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKOLSPGDRVLAADDQGRLLYSDFLTFL 242
Db 184 CSVKSEHSAAKTGGCFPGRALATLENGARTPLWALRPGQORVLAAMDGAGRPTYSDFLAFL 243
QY 243 DRDDGAKKVPYVIETREPRERLLITAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPR 302
Db 244 DKEPRALTAFHVIETRQPPRRALTPTHTLLFVA---DNA-----SAPAAQFR 287
QY 303 ALFASRVRCQORVVVAERDGDRLRLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLAS 362
Db 288 PTFASHVOPGHFVLVAV---GSGGLQPAEVVGV-GRITDVGAYAPLTRHGTLLVDDVVAS 343
QY 363 CYAVIEEHSWAHRAFAFRLAHALLAALAPARTDRGDSGGDRGGGGGRVALTAPGAAD 422
Db 344 CFALVREQLAQMAFWPLRLYHSL-----GGPGVQGD----- 376
QY 423 APGAGATAGTHWYSQLLYQIGTWLLDSEALHPLG 456
Db 377 -----GVHWYSGLLYRLGRMLLPDSEHPLG 402

RESULT 10
IHH_HUMAN
ID_IHH_HUMAN STANDARD; PRT; 411 AA.
AC Q14623; O43322; Q8N4B9;
DT 15-JUL-1999 (Rel. 38, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Indian hedgehog protein precursor (IHH) (HHG-2).
GN IHH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Tate G., Kishimoto K., Mitsuya T.;
RT "Expression of Sonic hedgehog and its receptor Patched/Smoothed in
human cancer cell lines and embryonic organs."
RL J. Biochem. Mol. Biol. Biophys. 4:27-34(2000).
[2]
SEQUENCE OF 95-411 FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Soares M.B., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
SEQUENCE OF 100-411 FROM N.A.
RP TISSUE=Fetal lung;
RX MEDLINE=96070431; PubMed=7590746;
RA Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T.,
RA Gastier J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C.E.,
RA Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.;

RT "Cloning, expression, and chromosomal location of SHH and IHH: two
human homologues of the Drosophila segment polarity gene hedgehog."
RL Genomics 28:44-51(1995).
[4]
RN SEQUENCE OF 124-172 FROM N.A.
RX MEDLINE=95236997; PubMed=7720571;
RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
RT "Products, genetic linkage and limb patterning activity of a murine
hedgehog gene."
RL Development 120:3339-3353(1994).
[5]
RN VARIANTS BDA1 LYS-95; GLU-100 AND LYS-131.
RX MEDLINE=21372448; PubMed=11455389;
RA Gao B., Guo J., She C., Shu A., Yang M., Tan Z., Yang X., Guo S.,
RA Feng G., He L.;
RT "Mutations in IHH, encoding Indian hedgehog, cause brachydactyly type
A-1."
RL Nat. Genet. 28:386-388(2001).
[6]
RN VARIANT BDA1 ASN-100.
RX MEDLINE=22271632; PubMed=12384778;
RA McCready M.E., Sweeney E., Fryer A.E., Donnai D., Baig A., Racacho L.,
RA Warman M.L., Hunter A.G.W., Bulman D.E.;
RT "A novel mutation in the IHH gene causes brachydactyly type A1: a
95-year-old mystery resolved."
RL Hum. Genet. 111:368-375(2002).
[7]
RN VARIANTS ACFD LEU-46 AND ALA-190.
RX MEDLINE=22534978; PubMed=12632327;
RA Hellemons J., Coucke P.J., Giedion A., De Paepe A., Kramer P.,
RA Beemer F., Mortier G.R.;
RT "Homozygous mutations in IHH cause acrocapitofemoral dysplasia, an
autosomal recessive disorder with cone-shaped epiphyses in hands and
hips."
RL Am. J. Hum. Genet. 72:1040-1046(2003).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN
ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH
AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION
OF PARATHYROID HORMONE-RELATED PROTEIN (PTHrP) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC LUNG, AND IN ADULT
KIDNEY AND LIVER.
CC -!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
CC -!- DISEASE: Defects in IHH are the cause of brachydactyly type A1
(BDA1) [MIM:112500]. BDA1 is an autosomal dominant disorder
characterized by middle phalanges of all the digits rudimentary or
fused with the terminal phalanges. The proximal phalanges of the
thumbs and big toes are short.
CC -!- DISEASE: Defects in IHH are a cause of acrocapitofemoral
dysplasia (ACFD) [MIM:607778]. ACFD is a disorder characterized by
short stature of variable severity with postnatal onset. The most
constant radiographic abnormalities are observed in the tubular
bones of the hands and in the proximal part of the femur. Cone-
shaped epiphyses or a similar epiphyseal configuration with
premature epimetaphyseal fusion result in shortening of the
skeletal components involved. Cone-shaped epiphyses were also
present to a variable extent at the shoulders, knees, and ankles.
CC -!- SIMILARITY: Belongs to the hedgehog family.

Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K.,
Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;
"Products, genetic linkage and limb patterning activity of a murine
hedgehog gene";
Development 120:3339-3353(1994).
-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN
ENDOCHONDRAL OSSIFICATION; MAY REGULATE THE BALANCE BETWEEN GROWTH
AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION
OF PARATHYROID HORMONE-RELATED PROTEIN (PTHrP).
-!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
cell, while the N-terminal peptide remains associated with the
cell surface. Is also secreted in either cleaved or uncleaved form
to mediate signaling to other cells (By similarity).
-!- TISSUE SPECIFICITY: IN THE EMBRYO, DETECTED IN THE DEVELOPING GUT,
THE GROWTH ZONE OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM
AND UROGENITAL SINUS. IN THE ADULT KIDNEY, FOUND IN PROXIMAL
CONVOLUTED AND PROXIMAL STRAIGHT TUBULE.
-!- DEVELOPMENTAL STAGE: Detected at 10 dpc in developing gut, at 14.5
days dpc in the cartilage primordium and in the developing
urogenital sinus. Expression increases with gestational age in
kidney and duodenum, becoming maximal in adulthood.
-!- PTM: The C-terminal domain displays an autophosphorylation activity
and a cholesterol transferase activity. Both activities result in
the cleavage of the full-length protein and covalent attachment of
a cholesterol moiety to the C-terminal of the newly generated N-
terminal fragment (N-product). This covalent modification appears
to play an essential role in restricting the spatial distribution
of the protein activity to the cell surface. The N-product is the
active species in both local and long-range signaling, whereas the
C-product has no signaling activity (By similarity).
-!- SIMILARITY: Belongs to the hedgehog family.

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or send an email to license@isb-sib.ch).

EMBL; U85610; AAB49692.1; ALT_INIT.
DR EMBL; X76291; CAA53923.1; --
DR HSSP; Q62226; 1VHH.
DR MEROPS; C46.003; --
DR MGD; MGI:96533; Ihh.
DR InterPro; IPR009045; Hedgehog/DD_pept.
DR InterPro; IPR003587; Hedgehog_hinhN.
DR InterPro; IPR003586; Hedgehog_hinhC.
DR InterPro; IPR000320; HH_signal.
DR InterPro; IPR006141; Intein S.
DR InterPro; IPR001767; Pept_C46_hinh.
DR InterPro; IPR001657; Peptidase_C46.
DR Pfam; PF01085; HH_signal; 1.
DR Pfam; PF01079; Hint; 1.
DR PRINTS; PR00632; SONICHHOG.
DR ProDom; PD003042; HH_signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 411 INDIAN HEDGEHOG PROTEIN.
FT CHAIN 28 202 INDIAN HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 203 411 INDIAN HEDGEHOG PROTEIN C-PRODUCT.
FT SITE 202 203 CLEAVAGE (AUTO-).
FT SITE 248 248 INVOLVED IN CHOLESTEROL TRANSFER (BY
SIMILARITY).
FT SITE 272 272 INVOLVED IN AUTO-CLEAVAGE (BY
SIMILARITY).

FT ACT_SITE 275 275 ESSENTIAL FOR AUTO-CLEAVAGE (BY
FT LIPID 28 28 N-palmitoyl cysteine (By similarity).
FT LIPID 202 202 Cholesterol glycine ester (By
FT CONFLICT 383 383 W -> S (IN REF. 2).
SQ SEQUENCE 411 AA; 45485 MW; 08BE7AD8507C0D9B CRC64;
Query Match 51.1%; Score 1262; DB 1; Length 411;
Best Local Similarity 56.9%; Pred. No. 8.1e-84;
Matches 264; Conservative 46; Mismatches 86; Indels 68; Gaps 10;
QY 7 CLLVLVSSLLVCSGLACGPRGFG-KRRHPKKLTPLAYKQFIPNVAEKTGLGSGRYEGK 65
Db 13 CLFLLLL--LLVPAARGCGPRVVGSRPPRKLVLPLAYKQFSPNVPEKTGLGSGRYEGK 70
QY 66 ISRNSERFKELTPNPNPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQWPGVKLRVT 125
Db 71 IARSSERFKELTPNPNPDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQWPGVKLRVT 130
QY 126 EGWDEDEGHSEESLHYEGRAVDITTSDDRSKYGLMLARLAVEAGFDWVYVESKAHHCVS 185
Db 131 EGWDEDEGHSEESLHYEGRAVDITTSDDRNKYGLLARLAVEAGFDWVYVESKAHHCVS 190
QY 186 KAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLFLDRD 245
Db 191 KSEHSAAKTGGCFPAGAQVRLNGERVALSAVKPGDRVLAMGEDGTFPSDVLFLDRE 250
QY 246 DGAKKVFYVIETREPRERLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF 305
Db 251 PNRLRAFQVIETQDPFRRLLALTPAHLFLIA--DNHT-EPAAHF-----RATF 294
QY 306 ASVRPQGVVVAERDGRRLPAAVHVSITLSEEAAGAYAPLTAQGTILINRVLASCYA 365
Db 295 ASHVQPGQVVLV---SGVPGLOPARVAVS-THVALGSVAPLTHRGTLVVEDVVASCPA 349
QY 366 VIEHSHWAHRAFPRLAHALL-AALAPARTDRGDSGGDRGGGRVALTAPGAADAP 424
Db 350 AVADHHLAQLAFWPLRLFPPLAWSWTFPSE-----
QY 425 GAGATAGIHWYSOLLQYQIGTWLLDSEALHPLGMVAVKSSXSRGAG 468
Db 380 -----GVHWYPQMLYRLGRLLLEESTFHLGMS-----GAG 410
RESULT 12
IHH_XENLA
ID IHH_XENLA STANDARD; PRT; 409 AA.
AC Q91612;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Indian hedgehog protein precursor (IHH) (Banded hedgehog protein) (X-
BHH).
GN IHH OR BHH.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=95401852; PubMed=7671800;
RA Ekker S.C., McGrew L.L., Lai C.-J., Lee J.J., von Kessler D.P.,
RA Moon R.T., Beachy P.A.;
RT "Distinct expression and shared activities of members of the hedgehog
RT gene family of Xenopus laevis."
RL Development 121:2337-2347(1995).
CC -!- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF
CC ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC
CC CEMENT GLAND FORMATION IN EMBRYOS.
CC -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE

| | | | |
|--|--|----|--|
| DR | MEROPS; C46.004; -- | DR | MEEROPS; C46.004; -- |
| DR | MGD; MGI:94891; Dnh. | DR | MGD; MGI:94891; Dnh. |
| DR | InterPro; IPR009045; Hedgehog/DD_pept. | DR | InterPro; IPR009045; Hedgehog/DD_pept. |
| DR | InterPro; IPR003587; Hedgehog_hint N. | DR | InterPro; IPR003587; Hedgehog_hint N. |
| DR | InterPro; IPR003586; Hedgehog_hintC. | DR | InterPro; IPR003586; Hedgehog_hintC. |
| DR | InterPro; IPR000320; HH_signal. | DR | InterPro; IPR000320; HH_signal. |
| DR | InterPro; IPR006141; Intein_S. | DR | InterPro; IPR006141; Intein_S. |
| DR | InterPro; IPR001767; Pept C46 hint. | DR | InterPro; IPR001767; Pept C46 hint. |
| DR | InterPro; IPR001657; Peptidase_C46. | DR | InterPro; IPR001657; Peptidase_C46. |
| DR | Pfam; PF01085; HH_signal; 1. | DR | Pfam; PF01085; HH_signal; 1. |
| DR | Pfam; PF01079; Hint; 1. | DR | Pfam; PF01079; Hint; 1. |
| DR | PRINTS; PR00632; SONICHHOG. | DR | PRINTS; PR00632; SONICHHOG. |
| DR | ProDom; PD003042; HH_signal; 1. | DR | ProDom; PD003042; HH_signal; 1. |
| DR | SMART; SM00305; HintC; 1. | DR | SMART; SM00305; HintC; 1. |
| DR | SMART; SM00306; HintN; 1. | DR | SMART; SM00306; HintN; 1. |
| DR | PROSITE; PS00817; INTEIN_N_TER; 1. | DR | PROSITE; PS00817; INTEIN_N_TER; 1. |
| KW | Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; | KW | Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; |
| KW | Signal; Lipoprotein; Palmitate. | KW | Signal; Lipoprotein; Palmitate. |
| FT | SIGNAL 1 22 POTENTIAL. | FT | SIGNAL 1 22 POTENTIAL. |
| FT | CHAIN 23 396 DESERT HEDGEHOG PROTEIN. | FT | CHAIN 23 396 DESERT HEDGEHOG PROTEIN. |
| FT | CHAIN 23 198 DESERT HEDGEHOG PROTEIN N-PRODUCT. | FT | CHAIN 23 198 DESERT HEDGEHOG PROTEIN N-PRODUCT. |
| FT | CHAIN 199 396 DESERT HEDGEHOG PROTEIN C-PRODUCT. | FT | CHAIN 199 396 DESERT HEDGEHOG PROTEIN C-PRODUCT. |
| FT | SITE 198 199 CLEAVAGE (AUTO-). | FT | SITE 198 199 CLEAVAGE (AUTO-). |
| FT | SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY | FT | SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY |
| FT | SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY | FT | SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY |
| FT | ACT_SITE 271 271 SIMILARITY). | FT | ACT_SITE 271 271 SIMILARITY). |
| FT | LIPID 23 23 N-palmitoyl cysteine (By similarity). | FT | LIPID 23 23 N-palmitoyl cysteine (By similarity). |
| FT | LIPID 198 198 Cholesterol glycine ester (By | FT | LIPID 198 198 Cholesterol glycine ester (By |
| SQ | SEQUENCE 396 AA; 43542 MW; AFEB051BE950FD8 CRC64; | SQ | SEQUENCE 396 AA; 43542 MW; AFEB051BE950FD8 CRC64; |
| Query Match 47.9%; Score 1183; DB 1; Length 396; | | | |
| Best Local Similarity 54.5%; Pred. No. 3.9e-78; | | | |
| Matches 244; Conservative 55; Mismatches 87; Indels 62; Gaps 10; | | | |
| QY | 3 LLARCLLLVSSLLVCSGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTGLGSG 60 | QY | 3 LLARCLLLVSSLLVCSGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTGLGSG 60 |
| Db | 7 LPLCLCL-----ALLLSAQSCGPGRGVGRRRYVRKQLVPLLYKQFVPSMPERTLGASG 61 | Db | 7 LPLCLCL-----ALLLSAQSCGPGRGVGRRRYVRKQLVPLLYKQFVPSMPERTLGASG 61 |
| QY | 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 120 | QY | 61 RYEGKISRNSERFKELTPNYPNDIIFKDEENTGADRLMTQCKDKLNALAI SVMNQPGV 120 |
| Db | 62 PAEGRVTRGSEFRDLVFNYPNDIIFKDEENSGADRLMTQCKDKLNALAI SVMNQPGV 121 | Db | 62 PAEGRVTRGSEFRDLVFNYPNDIIFKDEENSGADRLMTQCKDKLNALAI SVMNQPGV 121 |
| QY | 121 KLRVTEGWDEGDHSHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180 | QY | 121 KLRVTEGWDEGDHSHSESLHYEGRAVDITTSDDRSKYGMLARLAVEAGFDWVYESKAH 180 |
| Db | 122 PLRVTEGWDEGDHHAQDSLHYEGRALDITTSDDRNKYGLLARLAVEAGFDWVYESRHH 181 | Db | 122 PLRVTEGWDEGDHHAQDSLHYEGRALDITTSDDRNKYGLLARLAVEAGFDWVYESRHH 181 |
| QY | 181 IHCSVKAENSVAKSGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240 | QY | 181 IHCSVKAENSVAKSGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240 |
| Db | 182 IHVSVKADNSLAVRAGGCFPGNATVRLSRGERKGLRELHGRDWTVLADAAAGRVVTPVLL 241 | Db | 182 IHVSVKADNSLAVRAGGCFPGNATVRLSRGERKGLRELHGRDWTVLADAAAGRVVTPVLL 241 |
| QY | 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGP-PSGGAL 299 | QY | 241 FLDRDDGAKKVFYVETREPRERLLLTAHLLFVAPHNDSATGEPEASSGSGP-PSGGAL 299 |
| Db | 242 FLDRDLQRRASFVAVETERPPRKLTLTPWHLVFAA-----RGAPAPGDF 286 | Db | 242 FLDRDLQRRASFVAVETERPPRKLTLTPWHLVFAA-----RGAPAPGDF 286 |
| QY | 300 GPRALFASRVPRGQVVVVAERDGRRLLPAAVHVSITLSEEAAGAYAPLTAQGTILINRV 359 | QY | 300 GPRALFASRVPRGQVVVVAERDGRRLLPAAVHVSITLSEEAAGAYAPLTAQGTILINRV 359 |
| Db | 287 AP--VFARRLRAGDSVLA----PGGDALQPARVARVA-REEAVGVFAPLTAHGTLLVNDV 339 | Db | 287 AP--VFARRLRAGDSVLA----PGGDALQPARVARVA-REEAVGVFAPLTAHGTLLVNDV 339 |
| QY | 360 LASCYAVIEHSHWAHAFAPFRLLAHALLAALAPARTDRGGSGGDRGGGGRVALTAPG 419 | QY | 360 LASCYAVIEHSHWAHAFAPFRLLAHALLAALAPARTDRGGSGGDRGGGGRVALTAPG 419 |
| Db | 340 LASCYAVLESHQWAHAFAPRLRLHALGALL-----PG 372 | Db | 340 LASCYAVLESHQWAHAFAPRLRLHALGALL-----PG 372 |
| QY | 420 AADAPGAGATAGIHWSQLLYQIGTWLL 447 | QY | 420 AADAPGAGATAGIHWSQLLYQIGTWLL 447 |
| Db | 373 GAVQP-----TGMHWYSRLLYRLABELM 395 | Db | 373 GAVQP-----TGMHWYSRLLYRLABELM 395 |
| RESULT 15 | | | |
| DHH_HUMAN | | | |

| | | | | |
|----|---|-----------|------|---------|
| ID | DHH_HUMAN | STANDARD; | PRT; | 396 AA. |
| AC | O43323; Q15794; | | | |
| DT | 15-JUL-1999 (Rel. 38, Created) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last sequence update) | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Desert hedgehog protein precursor (DHH) (HHG-3). | | | |
| GN | DHH. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Tate G., Kishimoto K., Mitsuya T.; | | | |
| RT | "Expression of Sonic hedgehog and its receptor Patched/Smoothed in | | | |
| RT | human cancer cell lines and embryonic organs." | | | |
| RL | J. Biochem. Mol. Biol. Biophys. 4:27-34(2000). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Brain; | | | |
| RX | MEDLINE=22388257; PubMed=12477932; | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | | | |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., | | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | | | |
| RA | Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | |
| RA | Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., | | | |
| RA | Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., | | | |
| RA | Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; | | | |
| RT | "Generation and initial analysis of more than 15,000 full-length | | | |
| RT | human and mouse cDNA sequences." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | |
| RN | [3] | | | |
| RP | SEQUENCE OF 85-178 FROM N.A. | | | |
| RC | TISSUE=Kidney; | | | |
| RA | Drummond I.A.; | | | |
| RT | "Human desert hedgehog." | | | |
| RL | Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [4] | | | |
| RP | DISEASE. | | | |
| RX | MEDLINE=20489872; PubMed=11017805; | | | |
| RA | Umehara F., Tate G., Itoh K., Yamaguchi N., Douchi T., Mitsuya T., | | | |
| RA | Osame M.; | | | |
| RT | "A novel mutation of desert hedgehog in a patient with 46,XY partial | | | |
| RT | gonadal dysgenesis accompanied by minifascicular neuropathy." | | | |
| RL | Am. J. Hum. Genet. 67:1302-1305(2000). | | | |
| CC | -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF | | | |
| CC | PATTERNING EVENTS DURING DEVELOPMENT. MAY FUNCTION AS A | | | |
| CC | SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL FOR TESTES | | | |
| CC | DEVELOPMENT. | | | |
| CC | -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the | | | |
| CC | cell, while the N-terminal peptide remains associated with the | | | |
| CC | cell surface. Is also secreted in either cleaved or uncleaved form | | | |
| CC | to mediate signaling to other cells (By similarity). | | | |
| CC | -!- PTM: The C-terminal domain displays an autotranspeptidation | | | |
| CC | and a cholesterol transferase activity. Both activities result in | | | |
| CC | the cleavage of the full-length protein and covalent attachment of | | | |
| CC | a cholesterol moiety to the C-terminal of the newly generated N- | | | |
| CC | terminal fragment (N-product). This covalent modification appears | | | |
| CC | to play an essential role in restricting the spatial distribution | | | |
| CC | of the protein activity to the cell surface. The N-product is the | | | |
| CC | active species in both local and long-range signaling, whereas the | | | |
| CC | C-product has no signaling activity (By similarity). | | | |
| CC | -!- DISEASE: Defects in DHH may be the cause of partial gonadal | | | |

CC dysgenesis with minifascicular neuropathy 46.XY (PGD)
CC [MIM:607080]. PGD is characterized by the presence of a testis on
CC one side and a streak or an absent gonad at the other, persistence
CC of Mullerian duct structures, and a variable degree of genital
CC ambiguity.
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB010994; BAA24866.1; --
CC EMBL; AB010581; BAA24866.1; JOINED.
CC EMBL; AB010983; BAA24866.1; JOINED.
CC EMBL; BC033507; AAH33507.1; --
CC EMBL; U59748; AAB03398.1; --
CC PIR; G02735; G02735.
CC HSSP; Q62226; 1VHH.
CC MEROPS; C46.004; --
CC Genew; HGNC:2865; DHH.
CC MIM; 605423; --
CC MIM; 607080; --
CC InterPro; IPR009045; Hedgehog/DD_pept.
CC InterPro; IPR003587; Hedgehog_hint N.
CC InterPro; IPR003586; Hedgehog_hintC.
CC InterPro; IPR000320; HH_signal.
CC InterPro; IPR001767; Pept_C46_hint.
CC InterPro; IPR001657; Peptidase_C46.
CC Pfam; PF01085; HH_signal; 1.
CC Pfam; PF01079; Hint; 1.
CC PRINTS; PR00632; SONICHHOG.
CC ProDom; PD003042; HH_signal; 1.
CC SMART; SM00305; HintC; 1.
CC SMART; SM00306; HintN; 1.
CC Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
CC Signal; Lipoprotein; Palmitate.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 396 DESERT HEDGEHOG PROTEIN.
FT CHAIN 23 198 DESERT HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 199 396 DESERT HEDGEHOG PROTEIN C-PRODUCT.
FT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY
FT SIMILARITY).
FT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY
FT SIMILARITY).
FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY
FT SIMILARITY).
FT LIPID 23 23 N-palmitoyl cysteine (By similarity).
FT LIPID 198 198 Cholesterol glycine ester (By
FT similarity).
FT CONFLICT 177 177 E -> G (IN REF. 3).
SQ SEQUENCE 396 AA; 43577 MW; FCE4FE21972C3AD5 CRC64;

Query Match 47.7%; Score 1177; DB 1; Length 396;
Best Local Similarity 54.4%; Pred. No. 1.1e-77;
Matches 245; Conservative 54; Mismatches 93; Indels 58; Gaps 10;

QY 1 MLLLRCLLLVSVLLVCSGLACGPRG-FGKRRHPKK-LTFLAYKQFIPNVAEKLGA 58
DB 1 MALLTNLLPLCCL-ALLALPAQSCGPGRGVRRRYARKQLVLLYKQFVGPVPTLGA 59

QY 59 SGRYEGKISRNSERFKELTPNYPNPDIFKDEENTGADRLMTQRCCKLNALAI SVMNQWP 118
DB 60 SGPAEGRVARGSRFRDLVPNYPNPDIFKDEENSGADRLMTQRCCKERNALAI SVMNWP 119

QY 119 GVKLRVTEGWDEGHSEESLHYEGRAVDITTSDDRSKYGMRLARLAVEAGFDWVYVESK 178
DB 120 GVRLRVTEGWDEGHQAQDSLHYEGRALDITTSDDRNRKYGLLARLAVEAGFDWVYVESR 179

QY 179 AHIHCSVKAENSVAAKSGGCGPFGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDF 238
DB 180 NHVHVSVKADNSLAVRAGCGPFGNATVRLWSGERKGLRELHGRDWNVLAADASGRVYPTPV 239
QY 239 LTFLDRDDGAKKVFIYIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGP-PSGG 297
DB 240 LLFLDRDLQRRASFVAVETEWPRKLLLTWHLVFAA-----RGPAPAG 284
QY 298 ALGPRALFASRVPRGQVYVVAERDGDRLRLPAAVHVSVTLSAAAGAYAPLTAQGTILIN 357
DB 285 DFAP--VFARRLRAGDSVLA---PGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVN 337
QY 358 RVLASCYAVIEHSHWAHRAFAFAPRLAHALLAALAPARTDRGDSGGDRGGGGRVALTA 417
DB 338 DVLASCYAVLESHQWAHRAFAFAPRLHALLGALL----- 370
QY 418 PGAADAPGAGATAGIHWYSQLLYQIGTWLL 447
DB 371 PGGAVQP-----TGMHWYSRLLYRLAEELL 395

RESULT 16
DHH1_XENLA
ID DHH1_XENLA STANDARD; PRT; 396 AA.
AC Q91610;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Desert hedgehog protein precursor 1 (DHH-1) (Cephalic hedgehog
DE protein) (X-CHH).
GN CHH.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=95401852; PubMed=7671800;
RA Ekker S.C., McGrew L.L., Lai C.-J., Lee J.J., von Kessler D.P.,
RA Moon R.T., Beachy P.A.;
RT "Distinct expression and shared activities of members of the hedgehog
RT gene family of Xenopus laevis";
RL Development 121:2337-2347(1995).
CC -!- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF
CC ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC
CC CEMENT GLAND FORMATION IN EMBRYOS.
CC -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
CC CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED
CC OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY
CC SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE EARLY GASTRULA. IN THE
CC NEURULA EXPRESSION BECOMES RESTRICTED TO ANTERIOR STRUCTURES,
CC ENCOMPASSING BOTH NEURAL PLATE AND ENDODERMAL CELLS.
CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.
CC -----
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